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(54) Title: ANTI-BACTERIAL VACCINE COMPOSITIONS

(57) Abstract: Gram negative bacterial virulence genes are identified, thereby allowing the identification of novel anti-bacterial agents that target these virulence genes and their products, and the provision of novel gram negative bacterial mutants useful in vaccines.

## ANTI-BACTERIAL VACCINE COMPOSITIONS

This application is a continuation-in-part of U.S. Patent Application Serial No: 09/545,199, filed April 6, 2000, which claims benefit of U.S. Provisional Patent Application Serial Nos. 60/153,453, filed September 10, 1999 and 60/128,689, filed April 9, 1999.

### FIELD OF THE INVENTION

The present invention relates generally to the identification of genes responsible for virulence of *Pasteurellaceae* bacteria, thereby allowing for production of novel attenuated mutant strains useful in vaccines and identification of new anti-bacterial agents that target the virulence genes and their products.

### BACKGROUND OF THE INVENTION

The family *Pasteurellaceae* encompasses several significant pathogens that infect a wide variety of animals. In addition to *P. multocida*, prominent members of the family include *Pasteurella (Mannheimia) haemolytica*, *Actinobacillus pleuropneumoniae* and *Haemophilus somnus*. *P. multocida* is a gram-negative, nonmotile coccobacillus which is found in the normal flora of many wild and domestic animals and is known to cause disease in numerous animal species worldwide [Biberstein, In M. Kilian, W. Frederickson, and E. L. Biberstein (ed.), *Haemophilus, Pasteurella, and Actinobacillus*. Academic Press, London, p. 61-73 (1981)]. The disease manifestations following infection include septicemias, bronchopneumonias, rhinitis, and wound infections [Reviewed in Shewen, *et al.*, In C. L. Gyles and C. O. Thoen (ed.), Pathogenesis of Bacterial Infections in Animals. Iowa State University Press, Ames, p. 216-225 (1993), incorporated herein by reference].

Infection by *P. multocida* generally results from invasion during periods of stress, but transmission may also occur by aerosol or contact exposure, or via flea and tick vectors. In fowl, *P. multocida* infection gives rise to acute to peracute septicemia, particularly prevalent in domestic turkeys and wild waterfowl under stress conditions associated with overcrowding, laying, molting, or severe

climatic change. In cattle, a similar hemorrhagic septicemia follows infection and manifests conditions including high fever and depression, generally followed by quick death. Transmission is most likely through aerosol contact, but infection can also arise during periods of significant climatic change. In rabbits, infection gives rise to recurring purulent rhinitis, generally followed by conjunctivitis, otitis media, sinusitis, subcutaneous abscesses, and chronic bronchopneumonia. In severe infections, rabbit mortality arises from acute fibrinous bronchopneumonia, septicemia, or endotoxemia. Disease states normally arise during periods of stress. In pigs, common *P. multocida* disease states include atrophic rhinitis and bacterial pneumonia. Similar pneumonia conditions are also detected in dogs, cats, goats, and sheep. *P. multocida* is commonly detected in oral flora of many animals and is therefore a common contaminant in bite and scratch wounds.

*P. multocida* strains are normally designated by capsular serogroup and somatic serotype. Five capsular serogroups (A, B, D, E, and F) and 16 somatic serotypes are distinguished by expression of characteristic heat-stable antigens. Most strains are host specific and rarely infect more than one or two animals. The existence of different serotypes presents a problem for vaccination because traditional killed whole cell bacteria normally provide only serotype-specific protection. However, it has been demonstrated that natural infection with one serotype can lead to immunological protection against multiple serotypes [Shewen, *et al.*, In C. L. Gyles and C. O. Thoen (Ed.), Pathogenesis of Bacterial Infections in Animals. Iowa State University Press, Ames, p. 216-225 (1993)] and cross protection can also be stimulated by using inactivated bacteria grown *in vivo* [Rimler, *et al.*, *Am J Vet Res.* 42:2117-2121 (1981)]. One live spontaneous mutant *P. multocida* strain has been utilized as a vaccine and has been shown to stimulate a strong immune response [Davis, *Poultry Digest.* 20:430-434 (1987), Schlink, *et al.*, *Avian Dis.* 31(1):13-21 (1987)]. This attenuated strain, however, has been shown to revert to a virulent state or cause mortality if the vaccine recipient is stressed [Davis, *Poultry Digest.* 20:430-434 (1987), Schlink, *et al.*, *Avian Dis.* 31(1):13-21 (1987)].

Another member of the *Pasteurella* family, *A. pleuropneumoniae* exhibits strict host specificity for swine and is the causative agent of highly contagious porcine pleuropneumonia. Infection normally arises in intensive breeding conditions, and is believed to occur by a direct mode of transmission. The disease is often fatal and, as a result, leads to severe economic loss in the swine producing industry. *A. pleuropneumoniae* infection may be chronic or acute, and infection is characterized by a hemorrhagic, necrotic bronchopneumonia with accompanying fibrinous pleuritis. To date, bacterial virulence has been attributed to structural proteins, including serotype-specific capsular polysaccharides, lipopolysaccharides, and surface proteins, as well as extracellular cytolytic toxins. Despite purification and, in some instances cloning, of these virulence factors, the exact role of these virulence factors in *A. pleuropneumoniae* infection is poorly understood.

Twelve serotypes of *A. pleuropneumoniae* have been identified based on antigenic differences in capsular polysaccharides and production of extracellular toxins. Serotypes 1, 5, and 7 are most relevant to *A. pleuropneumoniae* infection in the United States, while serotypes 1, 2, 5, 7, and 9 are predominant in Europe. There are at least three significant extracellular toxins of *A. pleuropneumoniae* that are members of the haemolysin family and are referred to as RTX toxins. RTX toxins are produced by many Gram negative bacteria, including *E. coli*, *Proteus vulgaris*, and *Pasteurella haemolytica*, and the proteins generally share structural and functional characteristics. Toxins from the various serotypes differ, however, in host specificity, target cells, and biological activities.

The major *A. pleuropneumoniae* RTX toxins include ApxI, ApxII, and ApxIII. ApxI and ApxII have haemolytic activity, with ApxI being more potent. ApxIII shows no haemolytic activity, but is cytotoxic for alveolar macrophages and neutrophils. Most *A. pleuropneumoniae* serotypes produce two of these three toxins. For example, serotypes 1, 5, 9, and 11 express ApxI and ApxII, and serotypes 2, 3, 4, 6, and 8 express ApxII and ApxIII. Serotype 10, however, produces only ApxI, and serotypes 7 and 12 express only ApxII. Those *A. pleuropneumoniae* serotypes that produce both ApxI and ApxII are the most virulent strains of the bacteria.



The Apx toxins were demonstrated to be virulence factors in murine models and swine infection using randomly mutated wild type bacteria [Tascon, *et al.*, *Mol. Microbiol.* 14:207-216 (1994)]. Other *A. pleuropneumoniae* mutants have also been generated with targeted mutagenesis to inactivate the gene encoding the AopA outer membrane virulence protein [Mulks and Buysee, *Gene* 165:61-66 (1995)].

At least eleven serotypes (1, 2, 5-9, 12-14 and 16) have been demonstrated within *Mannheimia [Pasteurella] haemolytica* [Angen, *et al.*, *Vet Microbiol* 65(4):283-90 (1999)], a *Pasteurellaceae* species which is responsible for serious outbreaks of acute pneumonia in neonatal, weaned, growing and adult lambs, calves, and goats [Ackermann, *et al.*, *Microbes Infect* 2(9):1079-88 (2000)]. Transportation, viral infections, overcrowding, and other stressful conditions predispose animals to *M. haemolytica* infection [Ackermann, *et al.*, *supra.*] The leukotoxin (Lkt) of *M. haemolytica* is believed to play a significant role in pathogenesis, causing cell lysis and apoptosis that lead to the lung pathology characteristic of bovine shipping fever [Highlander, *et al.*, *Infect Immun* 68(7):3916-22 (2000)] as well as lung injury in bovine pneumonic pasteurellosis [Jeyaseelan, *et al.*, *Microb Pathog* 30(2):59-69 (2001)]. Lkt is a pore-forming exotoxin that has the unique property of inducing cytolysis only in ruminant leukocytes and platelets [Jeyaseelan, *et al.*, (2001), *supra.*]. Cytolysis of many cell types is mediated by arachidonic acid (AA) and its generation by phospholipases is regulated by G-protein-coupled receptors [Jeyaseelan, *et al.*, (2001) *supra.*] Recent studies indicate that *M. haemolytica* Lkt binds to bovine CD18, the common subunit of all beta2 integrins [Jeyaseelan, *et al.*, *Infect Immun* 68(1):72-9 (2000)]. It has also been shown that LFA-1 is a Lkt receptor, Lkt binding to LFA-1 is not target cell specific, Lkt binding to bovine LFA-1 correlates with calcium elevation and cytolysis, and bovine LFA-1 expression correlates with the magnitude of Lkt-induced target cell cytolysis [Jeyaseelan, *et al.*, *Infect Immun* 68(1):72-9 (2000)].

In attempts to produce vaccine compositions, traditional killed whole cell bacteria have provided only serotype-specific protection [MacInnes and Smart, *supra.*], however, it has been demonstrated that natural infection with a highly virulent

serotype can stimulate strong protective immunity against multiple serotypes [Nielsen, *Nord Vet Med.* 31:407-13 (1979), Nielsen, *Nord Vet Med.* 36:221-234 (1984), Nielsen, *Can J Vet Res.* 29:580-582 (1988), Nielsen, *ACTA Vet Scand.* 15:80-89 (1994)]. One defined live-attenuated vaccine strain producing an inactive form of the ApxII toxin has shown promise for cross protection in swine [Prideaux, *et al.*, *Infection & Immunity* 67:1962-1966 (1999)], while other undefined live-attenuated mutants have also shown promise [Inzana, *et al.*, *Infect Immun.* 61:1682-6, (1993), Paltineanu, *et al.*, *In International Pig Veterinary Society*, 1992, p. 214, Utrera, *et al.*, *In International Pig Veterinary Society*, 1992, p. 213].

Because of the problems associated with vaccine formulations comprising bacterial strains with undefined, spontaneous mutations, there exists a need in the art for rational construction of live attenuated bacterial strains for use in vaccines that will safely stimulate protective immunity against homologous and heterologous *Pasteurellaceae* serotypes. There further exists a need to identify attenuated bacterial strains and genes required for bacterial virulence, thereby facilitating development of methods to identify anti-bacterial agents.

### SUMMARY OF THE INVENTION

In general, the present invention provides materials and methods for production and use of vaccine compositions comprising attenuated gram negative bacteria. In one aspect, vaccine compositions of the invention comprise attenuated species in the *Pasteurellaceae* family of bacteria, which is known in the art and described, in part, in Dewhirst, *et al.*, *J. Bacteriol.* 174:2002-2013 (1992), incorporated herein by reference in its entirety. Species in the family include, but are not limited to, *A. actinomycetemcomitans*, *A. capsulatus*, *A. equuli*, *A. lignieresii*, *A. pleuropneumoniae* (*H. pleuropneumoniae*), *A. seminis*, *A. suis* (*H. suis*), *A. ureae* (*p. ureae*), *A. capsulatus*, Bisgaard taxon 11, *H. aegyptius*, *H. aphrophilus*, *H. aphrophilus* (*H. parainfluenzae*), *H. ducreyi*, *H. haemoglobinophilus*, *H. haemolyticus*, *H. influenzae*, *H. paracuniculus*, *H. paragallinarum*, *H. parahaemolyticus*, *H. parainfluenzae*, (*H. paraphrophilus*), *H.*

*paraphrohaemolyticus*, *H. paraphrophilus*, *H. parasuis*, *H. parasuis* type 5, *H. segnis*,  
*H. somnus*, *Haemophilus* minor group, *Haemophilus* taxon C, *P. aerogenes*, *P. anatis*,  
*P. avium* (*H. avium*), *P. canis*, *P. dagmatis*, *P. gallinarum*, *P. (Mannheimia)*  
*haemolytica*, *P. trehalosi* (*P. haemolytica* biotype T), *P. langaa*, *P. multocida*, *P.*  
5 *pneumotropica*, *P. stomatis*, *P. volantium* (*H. parainfluenzae*), *P. volantium*,  
*Pasteurella* species A, *Pasteurella* species B, and *Haemophilus*  
*paraphrohaemolyticus*. Preferably, vaccine compositions comprise attenuated  
*Pasteurella (Mannheimia) haemolytica*, *Actinobacillus pleuropneumoniae*,  
*Haemophilus somnus*, or *Pasteurella multocida* bacteria. In a most preferred  
10 embodiment, vaccine compositions of the invention comprise attenuated *Pasteurella*  
*multocida* and *A. plueropneumoniae* bacterial strains.

One aspect of the invention provides gram negative bacterial  
 organisms containing a functional mutation in a gene sequence represented by any one  
 of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51,  
 15 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110,  
 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142,  
 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and  
 174, or species homologs thereof, wherein the mutation inhibits or abolishes  
 expression and/or biological activity of an encoded gene product (*i.e.*, the polypeptide  
 20 encoded by a gene); said functional mutation resulting in attenuated virulence of the  
 bacterial strain. Functional mutations that modulate (*i.e.*, increase or decrease)  
 expression and/or biological activity of a gene product include insertions or deletions  
 in the protein coding region of the gene itself or in sequences responsible for, or  
 involved in, control of gene expression. Deletion mutants include those wherein all or  
 25 part of a specific gene sequence is deleted. Also contemplated are compositions, and  
 preferably vaccine compositions, comprising mutated and attenuated gram negative  
 bacterial organisms, optionally comprising a suitable adjuvant and/or a  
 pharmaceutically acceptable diluent or carrier. In order for a modified strain to be  
 effective in a vaccine formulation, the attenuation must be significant enough to

prevent the pathogen from evoking severe clinical symptoms, but also insignificant enough to allow limited replication and growth of the bacteria in the host.

The invention also provides polynucleotides encoding gene products that are required for virulence in gram negative bacteria. Polynucleotides of the invention include DNA, such as complementary DNA, genomic DNA including  
5 complementary or anti-sense DNA, and wholly or partially synthesized DNA; RNA, including sense and antisense strands; and peptide nucleic acids as described, for example in Corey, *TIBTECH* 15:224-229 (1997). Virulence gene polynucleotides of the invention include those set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21,  
10 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or species homologs thereof, polynucleotides encoding a virulence gene product encoded by a polynucleotide of SEQ ID NOs: 1, 3,  
15 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or a species homolog thereof, and polynucleotide that hybridize, under moderately to highly stringent  
20 conditions, to the noncoding strand (or complement) of any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and  
25 174, or species homologs thereof. The invention therefore comprehends gene sequences from *Pasteurellaceae* set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162,  
30 163, 164, 166, 168, 170, 172, and 174, as well as related gene sequences from other

gram negative bacterial organisms, including naturally occurring (*i.e.*, species homologs) and artificially induced variants thereof. The invention also comprehends polynucleotides which encode polypeptides deduced from any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174, and species homologs thereof. Knowledge of the sequence of a polynucleotide of the invention makes readily available every possible fragment of that polynucleotide. The invention therefore provides fragments of a polynucleotide of the invention.

The invention further embraces expression constructs comprising polynucleotides of the invention. Host cells transformed, transfected or electroporated with a polynucleotide of the invention are also contemplated. The invention provides methods to produce a polypeptide encoded by a polynucleotide of the invention comprising the steps of growing a host cell of the invention under conditions that permit, and preferably promote, expression of a gene product encoded by the polynucleotide, and isolating the gene product from the host cell or the medium of its growth.

Identification of polynucleotides of the invention makes available the encoded polypeptides. Polypeptides of the invention include full length and fragment, or truncated, proteins; variants thereof; fusion, or chimeric proteins; and analogs, including those wherein conservative amino acid substitutions have been introduced into wild-type polypeptides. Antibodies that specifically recognize polypeptides of the invention are also provided, and include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, humanized antibodies, human antibodies, and complementary determining region (CDR)-grafted antibodies, as well as compounds that include CDR sequences which specifically recognize a polypeptide of the invention. The invention also provides anti-idiotypic antibodies immunospecific for antibodies of the invention.

According to another aspect of the invention, methods are provided for identifying novel anti-bacterial agents that modulate the function of gram negative bacteria virulence genes or gene products. Methods of the invention include screening potential agents for the ability to interfere with expression of virulence gene products encoded by the DNA sequences set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or species homologs thereof, or screening potential agents for the ability to interfere with biological function of a bacterial gene product encoded in whole or in part by a DNA sequence set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, species homologs thereof, or the complementary strand thereof, followed by identifying agents that provide positive results in such screening assays. In particular, agents that interfere with the expression of virulence gene products include anti-sense polynucleotides and ribozymes that are complementary to the virulence gene sequences. The invention further embraces methods to modulate transcription of gene products of the invention through use of oligonucleotide-directed triplet helix formation.

Agents that interfere with the function of virulence gene products include variants of virulence gene products, binding partners of the virulence gene products and variants of such binding partners, and enzyme inhibitors (where the product is an enzyme).

Novel anti-bacterial agents identified by the methods described herein are provided, as well as methods for treating a subject suffering from infection with gram negative bacteria involving administration of such novel anti-bacterial agents in an amount effective to reduce bacterial presence.

Numerous additional aspects and advantages of the invention will become apparent to those skilled in the art upon consideration of the following detailed description of the invention which describes presently prepared embodiments thereof.

5

### DETAILED DESCRIPTION OF THE INVENTION

"Virulence genes," as used herein, are genes whose function or products are required for successful establishment and/or maintenance of bacterial infection in a host animal. Thus, virulence genes and/or the proteins encoded thereby are involved in pathogenesis in the host organism, but may not be necessary for growth.

"Signature-tagged mutagenesis (STM)," as used herein, is a method generally described in International Patent Publication No. WO 96/17951, incorporated herein by reference, and includes, for example, a method for identifying bacterial genes required for virulence in a murine model of bacteremia. In this method, bacterial strains that each have a random mutation in the genome are produced using transposon integration; each insertional mutation carries a different DNA signature tag which allows mutants to be differentiated from each other. The tags comprise 40 bp variable central regions flanked by invariant "arms" of 20 bp which allow the central portions to be co-amplified by polymerase chain reaction (PCR). Tagged mutant strains are assembled in microtiter dishes, then combined to form the "inoculum pool" for infection studies. At an appropriate time after inoculation, bacteria are isolated from the animal and pooled to form the "recovered pool." The tags in the recovered pool and the tags in the inoculum pool are separately amplified, labeled, and then used to probe filters arrayed with all of the different tags representing the mutants in the inoculum. Mutant strains with attenuated virulence are those which cannot be recovered from the infected animal, *i.e.*, strains with tags that give hybridization signals when probed with tags from the inoculum pool but not when probed with tags from the recovered pool. In a variation of this method, non-radioactive detection methods such as chemiluminescence can be used

Signature-tagged mutagenesis allows a large number of insertional mutant strains to be screened simultaneously in a single animal for loss of virulence. Screening nineteen pools of mutant *P. multocida* strains resulted in the identification of more than 60 strains with reduced virulence, many of which were confirmed to be attenuated in virulence by subsequent determination of an approximate LD<sub>50</sub> for the individual mutants. Screening of *A. pleuropneumoniae* mutants resulted in identification of more than 100 strains having mutations in 35 different genes. Of these, mutations in 22 genes results in significantly attenuated *A. pleuropneumoniae* strains. The nucleotide sequence of the open reading frame disrupted by the transposon insertion was determined by sequencing both strands and an encoded amino acid sequence was deduced. Novelty of both the polynucleotide and amino acid sequences was determined by comparison of the sequences with DNA and protein database sequences. Knowledge of the virulence genes in these species permitted identification of species homologs in *P. (Mannheimia) haemolytica*.

The identification of bacterial, and more particularly *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence genes provides for microorganisms exhibiting reduced virulence (*i.e.*, attenuated strains), which are useful in vaccines. Such microorganisms include *Pasteurellaceae* mutants containing at least one functional mutation inactivating a gene represented by any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174. The worker of ordinary skill in the art will realize that a "functional mutation" may occur in protein coding regions of a gene of the invention, as well as in regulatory regions that modulate transcription of the virulence gene RNA.

The worker of ordinary skill will also appreciate that attenuated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* strains of the invention include those bearing more than one functional mutation. More than one mutation may result in additive or synergistic degrees of attenuation. Multiple



mutations can be prepared by design or may fortuitously arise from a deletion event originally intended to introduce a single mutation. An example of an attenuated strain with multiple deletions is a *Salmonella typhimurium* strain wherein the *cya* and *crp* genes are functionally deleted. This mutant *S. typhimurium* strain has shown promise as a live vaccine.

Identification of virulence genes in *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* can provide information regarding similar genes in other pathogenic species. As an example, identification of the *aroA* gene led to identification of conserved genes in a diverse number of pathogens, including *Aeromonas hydrophila*, *Aeromonas salmonicida*, *Salmonella typhimurium*, *Salmonella enteritidis*, *Salmonella dublin*, *Salmonella gallanum*, *Bordetella pertussis*, *Yersinia enterocolitica*, *Neisseria gonorrhoeae*, and *Bacillus anthracis*. In many of these species, attenuated bacterial strains bearing mutations in the *aroA* gene have proven to be effective in vaccine formulations. Using the virulence genes sequences identified in *P. multocida*, similar or homologous genes can be identified in other organisms, particularly within the *Pasteurella* family, as well as *A. pleuropneumoniae*, *P. (Mannheimia) haemolytica*, and *Haemophilus somnus*. Likewise, identification of *A. pleuropneumoniae* virulence genes can permit identification of related genes in other organisms. Southern hybridization using the *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* genes as probes can identify these related genes in chromosomal libraries derived from other organisms. Alternatively, PCR can be equally effective in gene identification across species boundaries. As still another alternative, complementation of, for example, a *P. multocida* mutant with a chromosomal library from other species can also be used to identify genes having the same or related virulence activity. Identification of related virulence genes can therefore lead to production of an attenuated strain of the other organism which can be useful as still another vaccine formulation. Examples of *P. multocida* genes that have been demonstrated to exist in other species (e.g. *P. (Mannheimia) haemolytica*, *A. pleuropneumoniae* and *H. somnus*) include genes *exxB*, *atpG*, *pnp*, *guaB* and *yjgF*.

Attenuated *P. multocida* strains identified using STM are insertional mutants wherein a virulence gene has been rendered non-functional through insertion of transposon sequences in either the open reading frame or regulatory DNA sequences. These insertional mutants still contain all of the genetic information  
5 required for bacterial virulence and can possibly revert to a pathogenic state by deletion of the inserted transposon. Therefore, in preparing a vaccine formulation, it is desirable to take the information gleaned from the attenuated strain and create a deletion mutant strain wherein some, most, or all of the virulence gene sequence is removed, thereby precluding the possibility that the bacteria will revert to a virulent  
10 state.

The vaccine properties of an attenuated insertional mutant identified using STM are expected to be the same or similar to those of a bacteria bearing a deletion in the same gene. However, it is possible that an insertion mutation may exert "polar" effects on adjoining gene sequences, and as a result, the insertion mutant  
15 may possess characteristic distinct from a mutant strain with a deletion in the same gene sequence. Deletion mutants can be constructed using any of a number of techniques well known and routinely practiced in the art.

In one example, a strategy using counterselectable markers can be employed which has commonly been utilized to delete genes in many bacteria. For a  
20 review, see, for example, Reyrat, *et al.*, *Infection and Immunity* 66:4011-4017 (1998), incorporated herein by reference. In this technique, a double selection strategy is often employed wherein a plasmid is constructed encoding both a selectable and counterselectable marker, with flanking DNA sequences derived from both sides of the desired deletion. The selectable marker is used to select for bacteria in which the  
25 plasmid has integrated into the genome in the appropriate location and manner. The counterselectable marker is used to select for the very small percentage of bacteria that have spontaneously eliminated the integrated plasmid. A fraction of these bacteria will then contain only the desired deletion with no other foreign DNA present. The key to the use of this technique is the availability of a suitable  
30 counterselectable marker.

In another technique, the *cre-lox* system is used for site specific recombination of DNA. The system consists of 34 base pair *lox* sequences that are recognized by the bacterial *cre* recombinase gene. If the *lox* sites are present in the DNA in an appropriate orientation, DNA flanked by the *lox* sites will be excised by the *cre* recombinase, resulting in the deletion of all sequences except for one remaining copy of the *lox* sequence. Using standard recombination techniques, it is possible to delete the targeted gene of interest in the *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* genome and to replace it with a selectable marker (e.g., a gene coding for kanamycin resistance) that is flanked by the *lox* sites. Transient expression (by electroporation of a suicide plasmid containing the *cre* gene under control of a promoter that functions in *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica*) of the *cre* recombinase should result in efficient elimination of the *lox* flanked marker. This process would result in a mutant containing the desired deletion mutation and one copy of the *lox* sequences.

In another approach, it is possible to directly replace a desired deleted sequence in the *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* genome with a marker gene, such as green fluorescent protein (GFP),  $\beta$ -galactosidase, or luciferase. In this technique, DNA segments flanking a desired deletion are prepared by PCR and cloned into a suicide (non-replicating) vector for *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica*. An expression cassette, containing a promoter active in *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica* and the appropriate marker gene, is cloned between the flanking sequences. The plasmid is introduced into wild-type *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica*. Bacteria that incorporate and express the marker gene (probably at a very low frequency) are isolated and examined for the appropriate recombination event (i.e., replacement of the wild type gene with the marker gene).

The reduced virulence of these organisms and their immunogenicity may be confirmed by administration to a subject animal. While it is possible for an avirulent microorganism of the invention to be administered alone, one or more of

such mutant microorganisms are preferably administered in a vaccine composition containing suitable adjuvant(s) and pharmaceutically acceptable diluent(s) or carrier(s). The carrier(s) must be "acceptable" in the sense of being compatible with the avirulent microorganism of the invention and not deleterious to the subject to be immunized. Typically, the carriers will be water or saline which will be sterile and pyrogen free. The subject to be immunized is a subject needing protection from a disease caused by a virulent form of *P. multocida*, *A. pleuropneumoniae*, *P. (Mannheimia) haemolytica* or other pathogenic microorganisms.

It will be appreciated that the vaccine of the invention may be useful in the fields of human medicine and veterinary medicine. Thus, the subject to be immunized may be a human or other animal, for example, farm animals including cows, sheep, pigs, horses, goats and poultry (e.g., chickens, turkeys, ducks and geese) companion animals such as dogs and cats; exotic and/or zoo animals; and laboratory animals including mice, rats, rabbits, guinea pigs, and hamsters.

The invention also provides polypeptides and corresponding polynucleotides required for *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* virulence. The invention includes both naturally occurring and non-naturally occurring polynucleotides and polypeptide products thereof. Naturally occurring virulence products include distinct gene and polypeptide species as well as corresponding species homologs expressed in organisms other than *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica* strains. Non-naturally occurring virulence products include variants of the naturally occurring products such as analogs and virulence products which include covalent modifications. In a preferred embodiment, the invention provides virulence polynucleotides comprising the sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof, and polypeptides having amino acids sequences encoded by the polynucleotides.

The present invention provides novel purified and isolated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* polynucleotides (e.g., DNA sequences and RNA transcripts, both sense and complementary antisense strands) encoding the bacterial virulence gene products. DNA sequences of the invention include genomic and cDNA sequences as well as wholly or partially chemically synthesized DNA sequences. Genomic DNA of the invention comprises the protein coding region for a polypeptide of the invention and includes variants that may be found in other bacterial strains of the same species. "Synthesized," as used herein and is understood in the art, refers to purely chemical, as opposed to enzymatic, methods for producing polynucleotides. "Wholly" synthesized DNA sequences are therefore produced entirely by chemical means, and "partially" synthesized DNAs embrace those wherein only portions of the resulting DNA were produced by chemical means. Preferred DNA sequences encoding *P. multocida* virulence gene products are set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, and species homologs thereof. Preferred *A. pleuropneumoniae* DNA sequences encoding virulence gene products are set out in SEQ ID NOs: 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof. Preferred *P. (Mannheimia) haemolytica* virulence gene products are set out in SEQ ID NOs: 166, 168, 170, 172 and 174, and species homologs thereof. The worker of skill in the art will readily appreciate that the preferred DNA of the invention comprises a double stranded molecule, for example, molecules having the sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof, along with the complementary molecule (the "non-coding strand" or "complement") having a sequence deducible from the sequence of SEQ ID NO: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53,

55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, according to Watson-Crick base pairing rules for DNA. Also preferred are

5 polynucleotides encoding the gene products encoded by any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166,

10 168, 170, 172, and 174 and species homologs thereof. The invention further embraces species, preferably bacterial, homologs of the *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* DNA.

The polynucleotide sequence information provided by the invention makes possible the identification and isolation of polynucleotides encoding related

15 bacterial virulence molecules by well known techniques including Southern and/or Northern hybridization, and polymerase chain reaction (PCR). Examples of related polynucleotides include polynucleotides encoding polypeptides homologous to a virulence gene product encoded by any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57,

20 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, and species homologs thereof, and structurally related polypeptides sharing one or more biological and/or physical properties of a virulence gene product of the invention.

25 The invention also embraces DNA sequences encoding bacterial gene products which hybridize under moderately to highly stringent conditions to the non-coding strand, or complement, of any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116,

30 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146,

148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174, and species homologs thereof. DNA sequences encoding virulence polypeptides which would hybridize thereto but for the degeneracy of the genetic code are contemplated by the invention. Exemplary high stringency conditions include a final wash in buffer  
5 comprising 0.2X SSC/0.1% SDS, at 65°C to 75°C, while exemplary moderate stringency conditions include a final wash in buffer comprising 2X SSC/0.1% SDS, at 35°C to 45°C. It is understood in the art that conditions of equivalent stringency can be achieved through variation of temperature and buffer, or salt concentration as described in Ausubel, *et al.* (Eds.), Protocols in Molecular Biology, John Wiley &  
10 Sons (1994), pp. 6.0.3 to 6.4.10. Modifications in hybridization conditions can be empirically determined or precisely calculated based on the length and the percentage of guanosine/cytosine (GC) base pairing of the probe. The hybridization conditions can be calculated as described in Sambrook, *et al.*, (Eds.), Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New  
15 York (1989), pp. 9.47 to 9.51.

Autonomously replicating recombinant expression constructions such as plasmid and viral DNA vectors incorporating virulence gene sequences are also provided. Expression constructs wherein virulence polypeptide-encoding polynucleotides are operatively linked to an endogenous or exogenous expression  
20 control DNA sequence and a transcription terminator are also provided. The virulence genes may be cloned by PCR, using *P. multocida* genomic DNA as the template. For ease of inserting the gene into expression vectors, PCR primers are chosen so that the PCR-amplified gene has a restriction enzyme site at the 5' end preceding the initiation codon ATG, and a restriction enzyme site at the 3' end after  
25 the termination codon TAG, TGA or TAA. If desirable, the codons in the gene are changed, without changing the amino acids, according to *E. coli* codon preference described by Grosjean and Fiers, *Gene*, 18:199-209 (1982), and Konigsberg and Godson, *Proc. Natl. Acad. Sci. (USA)*, 80:687-691 (1983). Optimization of codon usage may lead to an increase in the expression of the gene product when produced in  
30 *E. coli*. If the gene product is to be produced extracellularly, either in the periplasm of

*E. coli* or other bacteria, or into the cell culture medium, the gene is cloned without its initiation codon and placed into an expression vector behind a signal sequence.

According to another aspect of the invention, host cells are provided, including procaryotic and eukaryotic cells, either stably or transiently transformed, transfected, or electroporated with polynucleotide sequences of the invention in a manner which permits expression of virulence polypeptides of the invention.

Expression systems of the invention include bacterial, yeast, fungal, viral, invertebrate, and mammalian cells systems. Host cells of the invention are a valuable source of immunogen for development of antibodies specifically immunoreactive with the virulence gene product. Host cells of the invention are conspicuously useful in methods for large scale production of virulence polypeptides wherein the cells are grown in a suitable culture medium and the desired polypeptide products are isolated from the cells or from the medium in which the cells are grown by, for example, immunoaffinity purification or any of the multitude of purification techniques well known and routinely practiced in the art. Any suitable host cell may be used for expression of the gene product, such as *E. coli*, other bacteria, including *P. multocida*, *Bacillus* and *S. aureus*, yeast, including *Pichia pastoris* and *Saccharomyces cerevisiae*, insect cells, or mammalian cells, including CHO cells, utilizing suitable vectors known in the art. Proteins may be produced directly or fused to a peptide or polypeptide, and either intracellularly or extracellularly by secretion into the periplasmic space of a bacterial cell or into the cell culture medium. Secretion of a protein requires a signal peptide (also known as pre-sequence); a number of signal sequences from prokaryotes and eukaryotes are known to function for the secretion of recombinant proteins. During the protein secretion process, the signal peptide is removed by signal peptidase to yield the mature protein.

To simplify the protein purification process, a purification tag may be added either at the 5' or 3' end of the gene coding sequence. Commonly used purification tags include a stretch of six histidine residues (U.S. Patent Nos. 5,284,933 and 5,310,663), a streptavidin-affinity tag described by Schmidt and Skerra, *Protein Engineering*, 6:109-122 (1993), a FLAG peptide [Hopp *et al.*, *Biotechnology*, 6:1205-



1210 (1988)], glutathione S-transferase [Smith and Johnson, *Gene*, 67:31-40 (1988)], and thioredoxin [LaVallie *et al.*, *Bio/Technology*, 11:187-193 (1993)]. To remove these peptide or polypeptides, a proteolytic cleavage recognition site may be inserted at the fusion junction. Commonly used proteases are factor Xa, thrombin, and enterokinase.

The invention also provides purified and isolated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence polypeptides encoded by a polynucleotide of the invention. Presently preferred are polypeptides comprising the amino acid sequences encoded by any one of the polynucleotides set out in SEQ ID NOs : 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172 and 174, and species homologs thereof. The invention embraces virulence polypeptides encoded by a DNA selected from the group consisting of : a) the DNA sequence set out in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174 and species homologs thereof; b) DNA molecules encoding *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica*. polypeptides encoded by any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174, and species homologs thereof; and c) a DNA molecule, encoding a virulence gene product, that hybridizes under moderately stringent conditions to the DNA of (a) or (b).

The invention also embraces polypeptides that have at least about 99%, at least about 95%, at least about 90%, at least about 85%, at least about 80%, at least about 75%, at least about 70%, at least about 65%, at least about 60%, at least

about 55%, and at least about 50% identity and/or homology to the preferred polypeptides of the invention. Percent amino acid sequence "identity" with respect to the preferred polypeptides of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in the virulence gene product sequence after aligning both sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Percent sequence "homology" with respect to the preferred polypeptides of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in one of the virulence polypeptide sequences after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and also considering any conservative substitutions as part of the sequence identity. Conservative substitutions can be defined as set out in Tables A and B.

**Table A**  
**Conservative Substitutions I**

	<u>SIDE CHAIN CHARACTERISTIC</u>		<u>AMINO ACID</u>
20	Aliphatic	Non-polar	G A P I L V
		Polar - uncharged	C S T M N Q
		Polar - charged	D E K R
25	Aromatic		H F W Y
	Other		N Q D E

Polypeptides of the invention may be isolated from natural bacterial cell sources or may be chemically synthesized, but are preferably produced by recombinant procedures involving host cells of the invention. Virulence gene products of the invention may be full length polypeptides, biologically active fragments, or variants thereof which retain specific biological or immunological activity. Variants may comprise virulence polypeptide analogs wherein one or more

of the specified (*i.e.*, naturally encoded) amino acids is deleted or replaced or wherein one or more non-specified amino acids are added: (1) without loss of one or more of the biological activities or immunological characteristics specific for the virulence gene product; or (2) with specific disablement of a particular biological activity of the virulence gene product. Deletion variants contemplated also include fragments lacking portions of the polypeptide not essential for biological activity, and insertion variants include fusion polypeptides in which the wild-type polypeptide or fragment thereof have been fused to another polypeptide.

Variant virulence polypeptides include those wherein conservative substitutions have been introduced by modification of polynucleotides encoding polypeptides of the invention. Conservative substitutions are recognized in the art to classify amino acids according to their related physical properties and can be defined as set out in Table A (from WO 97/09433, page 10, published March 13, 1997 (PCT/GB96/02197, filed 9/6/96). Alternatively, conservative amino acids can be grouped as defined in Lehninger, [Biochemistry, Second Edition; Worth Publishers, Inc. NY:NY (1975), pp.71-77] as set out in Table B.

**Table B**  
**Conservative Substitutions II**

	<u>SIDE CHAIN</u> <u>CHARACTERISTIC</u>	<u>AMINO ACID</u>
	Non-polar (hydrophobic)	
	A. Aliphatic:	A L I V P
	B. Aromatic:	F W
	C. Sulfur-containing:	M
	D. Borderline:	G
	Uncharged-polar	
	A. Hydroxyl:	S T Y
	B. Amides:	N Q
	C. Sulfhydryl:	C
	D. Borderline:	G
	Positively Charged (Basic):	K R H
	Negatively Charged (Acidic):	D E

Variant virulence products of the invention include mature virulence gene products, *i.e.*, wherein leader or signal sequences are removed, having additional amino terminal residues. Virulence gene products having an additional methionine residue at position -1 are contemplated, as are virulence products having additional methionine and lysine residues at positions -2 and -1. Variants of these types are particularly useful for recombinant protein production in bacterial cell types. Variants of the invention also include gene products wherein amino terminal sequences derived from other proteins have been introduced, as well as variants comprising amino terminal sequences that are not found in naturally occurring proteins.

The invention also embraces variant polypeptides having additional amino acid residues which result from use of specific expression systems. For example, use of commercially available vectors that express a desired polypeptide as a fusion protein with glutathione-S-transferase (GST) provide the desired polypeptide having an additional glycine residue at position -1 following cleavage of the GST component from the desired polypeptide. Variants which result from expression using other vector systems are also contemplated.

Also comprehended by the present invention are antibodies (*e.g.*, monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, humanized, human, and CDR-grafted antibodies, including compounds which include CDR sequences which specifically recognize a polypeptide of the invention) and other binding proteins specific for virulence gene products or fragments thereof. The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind a virulence polypeptide exclusively (*i.e.*, are able to distinguish a single virulence polypeptides from related virulence polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see

Harlow *et al.* (Eds), Antibodies A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the virulence polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as  
5 defined above, a virulence polypeptide of the invention from which the fragment was derived.

The DNA and amino acid sequence information provided by the present invention also makes possible the systematic analysis of the structure and function of the virulence genes and their encoded gene products. Knowledge of a  
10 polynucleotide encoding a virulence gene product of the invention also makes available anti-sense polynucleotides which recognize and hybridize to polynucleotides encoding a virulence polypeptide of the invention. Full length and fragment anti-sense polynucleotides are provided. The worker of ordinary skill will appreciate that fragment anti-sense molecules of the invention include (i) those which  
15 specifically recognize and hybridize to a specific RNA (as determined by sequence comparison of DNA encoding a virulence polypeptide of the invention to DNA encoding other known molecules) as well as (ii) those which recognize and hybridize to RNA encoding variants of the family of virulence proteins. Antisense polynucleotides that hybridize to RNA encoding other members of the virulence  
20 family of proteins are also identifiable through sequence comparison to identify characteristic, or signature, sequences for the family of molecules.

The invention further contemplates methods to modulate gene expression through use of ribozymes. For a review, see Gibson and Shillitoe, *Mol. Biotech.* 7:125-137 (1997). Ribozyme technology can be utilized to inhibit translation  
25 of mRNA in a sequence specific manner through (i) the hybridization of a complementary RNA to a target mRNA and (ii) cleavage of the hybridized mRNA through nuclease activity inherent to the complementary strand. Ribozymes can be identified by empirical methods but more preferably are specifically designed based on accessible sites on the target mRNA [Bramlage, *et al.*, *Trends in Biotech* 16:434-  
30 438 (1998)]. Delivery of ribozymes to target cells can be accomplished using either

exogenous or endogenous delivery techniques well known and routinely practiced in the art. Exogenous delivery methods can include use of targeting liposomes or direct local injection. Endogenous methods include use of viral vectors and non-viral plasmids.

5                   Ribozymes can specifically modulate expression of virulence genes when designed to be complementary to regions unique to a polynucleotide encoding a virulence gene product. "Specifically modulate" therefore is intended to mean that ribozymes of the invention recognizes only a single polynucleotide. Similarly, ribozymes can be designed to modulate expression of all or some of a family of  
10                   proteins. Ribozymes of this type are designed to recognize polynucleotide sequences conserved in all or some of the polynucleotides which encode the family of proteins.

                  The invention further embraces methods to modulate transcription of a virulence gene of the invention through use of oligonucleotide-directed triplet helix formation. For a review, see Lavrovsky, *et al.*, *Biochem. Mol. Med.* 62:11-22 (1997).  
15                   Triplet helix formation is accomplished using sequence specific oligonucleotides which hybridize to double stranded DNA in the major groove as defined in the Watson-Crick model. Hybridization of a sequence specific oligonucleotide can thereafter modulate activity of DNA-binding proteins, including, for example, transcription factors and polymerases. Preferred target sequences for hybridization  
20                   include transcriptional regulatory regions that modulate virulence gene product expression. Oligonucleotides which are capable of triplet helix formation are also useful for site-specific covalent modification of target DNA sequences. Oligonucleotides useful for covalent modification are coupled to various DNA damaging agents as described in Lavrovsky, *et al.* [*supra*].

25                   The identification of *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence genes renders the genes and gene products useful in methods for identifying anti-bacterial agents. Such methods include assaying potential agents for the ability to interfere with expression of virulence gene products represented by the DNA sequences set forth in any one of SEQ ID NOS: 1,  
30                   3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68,

70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof (*i.e.*, the genes represented by DNA sequences of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 encode the virulence gene product, or the DNA sequences of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 are adjacent the gene encoding the virulence gene product, or are involved in regulation of expression of the virulence gene product), or assaying potential agents for the ability to interfere with the function of a bacterial gene product encoded in whole or in part by a DNA sequence set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, species homologs thereof, or the complementary strand thereof, followed by identifying agents that are positive in such assays. Polynucleotides and polypeptides useful in these assays include not only the genes and encoded polypeptides as disclosed herein, but also variants thereof that have substantially the same activity as the wild-type genes and polypeptides.

The virulence gene products produced by the methods described above are used in high throughput assays to screen for inhibitory agents. The sources for potential agents to be screened are chemical compound libraries, fermentation media of *Streptomyces*, other bacteria and fungi, and cell extracts of plants and other vegetations. For proteins with known enzymatic activity, assays are established based

on the activity, and a large number of potential agents are screened for ability to inhibit the activity. For proteins that interact with another protein or nucleic acid, binding assays are established to measure such interaction directly, and the potential agents are screened for ability to inhibit the binding interaction.

5                   The use of different assays known in the art is contemplated according to this aspect of the invention. When the function of the virulence gene product is known or predicted by sequence similarity to a known gene product, potential inhibitors can be screened in enzymatic or other types of biological and/or biochemical assays keyed to the function and/or properties of the gene product. When  
10   the virulence gene product is known or predicted by sequence similarity to a known gene product to interact with another protein or nucleic acid, inhibitors of the interaction can be screened directly in binding assays. The invention contemplates a multitude of assays to screen and identify inhibitors of binding by the virulence gene product. In one example, the virulence gene product is immobilized and interaction  
15   with a binding partner is assessed in the presence and absence of a putative inhibitor compound. In another example, interaction between the virulence gene product and its binding partner is assessed in a solution assay, both in the presence and absence of a putative inhibitor compound. In both assays, an inhibitor is identified as a compound that decreases binding between the virulence gene product and its binding  
20   partner. Other assays are also contemplated in those instances wherein the virulence gene product binding partner is a protein. For example, variations of the di-hybrid assay are contemplated wherein an inhibitor of protein/protein interactions is identified by detection of a positive signal in a transformed or transfected host cell as described in PCT publication number WO 95/20652, published August 3, 1995.

25                   Candidate inhibitors contemplated by the invention include compounds selected from libraries of potential inhibitors. There are a number of different libraries used for the identification of small molecule modulators, including: (1) chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules. Chemical  
30   libraries consist of structural analogs of known compounds or compounds that are



identified as "hits" or "leads" via natural product screening. Natural product libraries are collections of microorganisms, animals, plants, or marine organisms which are used to create mixtures for screening by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of plants or marine organisms. Natural product libraries include polyketides, non-ribosomal peptides, and variants (non-naturally occurring) thereof. For a review, see *Science* 282:63-68 (1998). Combinatorial libraries are composed of large numbers of peptides, oligonucleotides, or organic compounds as a mixture. They are relatively easy to prepare by traditional automated synthesis methods, PCR, cloning, or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to modulate activity.

Still other candidate inhibitors contemplated by the invention can be designed and include soluble forms of binding partners, as well as binding partners as chimeric, or fusion, proteins. Binding partners as used herein broadly encompasses antibodies, antibody fragments, and modified compounds comprising antibody domains that are immunospecific for the expression product of the identified virulence gene.

Other assays may be used when a binding partner (*i.e.*, ligand) for the virulence gene product is not known, including assays that identify binding partners of the target protein through measuring direct binding of test binding partner to the target protein, and assays that identify binding partners of target proteins through affinity ultrafiltration with ion spray mass spectroscopy/HPLC methods or other physical and analytical methods. Alternatively, such binding interactions are evaluated indirectly using the yeast two-hybrid system described in Fields and Song, *Nature*, 340:245-246 (1989), and Fields and Sternglanz, *Trends in Genetics*, 10:286-292 (1994), both of

which are incorporated herein by reference. The two-hybrid system is a genetic assay for detecting interactions between two proteins or polypeptides. It can be used to identify proteins that bind to a known protein of interest, or to delineate domains or residues critical for an interaction. Variations on this methodology have been developed to clone genes that encode DNA-binding proteins, to identify peptides that bind to a protein, and to screen for drugs. The two-hybrid system exploits the ability of a pair of interacting proteins to bring a transcription activation domain into close proximity with a DNA-binding domain that binds to an upstream activation sequence (UAS) of a reporter gene, and is generally performed in yeast. The assay requires the construction of two hybrid genes encoding (1) a DNA-binding domain that is fused to a first protein and (2) an activation domain fused to a second protein. The DNA-binding domain targets the first hybrid protein to the UAS of the reporter gene; however, because most proteins lack an activation domain, this DNA-binding hybrid protein does not activate transcription of the reporter gene. The second hybrid protein, which contains the activation domain, cannot by itself activate expression of the reporter gene because it does not bind the UAS. However, when both hybrid proteins are present, the noncovalent interaction of the first and second proteins tethers the activation domain to the UAS, activating transcription of the reporter gene. When the virulence gene product (the first protein, for example) is already known to interact with another protein or nucleic acid, this assay can be used to detect agents that interfere with the binding interaction. Expression of the reporter gene is monitored as different test agents are added to the system; the presence of an inhibitory agent results in lack of a reporter signal.

When the function of the virulence gene product is unknown and no ligands are known to bind the gene product, the yeast two-hybrid assay can also be used to identify proteins that bind to the gene product. In an assay to identify proteins that bind to the first protein (the target protein), a large number of hybrid genes each encoding different second proteins are produced and screened in the assay. Typically, the second protein is encoded by a pool of plasmids in which total cDNA or genomic DNA is ligated to the activation domain. This system is applicable to a wide variety

of proteins, and it is not even necessary to know the identity or function of the second binding protein. The system is highly sensitive and can detect interactions not revealed by other methods; even transient interactions may trigger transcription to produce a stable mRNA that can be repeatedly translated to yield the reporter protein.

5                   Other assays may be used to search for agents that bind to the target protein. One such screening method to identify direct binding of test ligands to a target protein is described in U.S. Patent No. 5,585,277, incorporated herein by reference. This method relies on the principle that proteins generally exist as a mixture of folded and unfolded states, and continually alternate between the two  
10                   states. When a test ligand binds to the folded form of a target protein (i.e., when the test ligand is a ligand of the target protein), the target protein molecule bound by the ligand remains in its folded state. Thus, the folded target protein is present to a greater extent in the presence of a test ligand which binds the target protein, than in the absence of a ligand. Binding of the ligand to the target protein can be determined  
15                   by any method which distinguishes between the folded and unfolded states of the target protein. The function of the target protein need not be known in order for this assay to be performed. Virtually any agent can be assessed by this method as a test ligand, including, but not limited to, metals, polypeptides, proteins, lipids, polysaccharides, polynucleotides and small organic molecules.

20                   Another method for identifying ligands for a target protein is described in Wieboldt *et al.*, *Anal. Chem.*, 69:1683-1691 (1997), incorporated herein by reference. This technique screens combinatorial libraries of 20-30 agents at a time in solution phase for binding to the target protein. Agents that bind to the target protein are separated from other library components by centrifugal ultrafiltration. The  
25                   specifically selected molecules that are retained on the filter are subsequently liberated from the target protein and analyzed by HPLC and pneumatically assisted electrospray (ion spray) ionization mass spectroscopy. This procedure selects library components with the greatest affinity for the target protein, and is particularly useful for small molecule libraries.

The inhibitors/binders identified by the initial screens are evaluated for their effect on virulence in *in vivo* mouse models of *P. multocida* infections. Models of bacteremia, endocarditis, septic arthritis, soft tissue abscess, or pneumonia may be utilized. Models involving use of other animals are also comprehended by the invention. For example, rabbits can be challenged with a wild type *P. multocida* strain before or after administration of varying amounts of a putative inhibitor/binder compound. Control animals, administered only saline instead of putative inhibitor/binder compound provide a standard by which deterioration of the test animal can be determined. Other animal models include those described in the Animal and Plant Health Inspection Service, USDA, January 1, 1994 Edition, §§113.69-113.70; Panciera and Corstvet, *Am. J. Vet. Res.* 45:2532-2537; Ames, *et al.*, *Can. J. Comp. Med.* 49:395-400 (1984); and Mukkur, *Infection and Immunity* 18:583-585 (1977). Inhibitors/binders that interfere with bacterial virulence are can prevent the establishment of an infection or reverse the outcome of an infection once it is established.

Any adjuvant known in the art may be used in the vaccine composition, including oil-based adjuvants such as Freund's Complete Adjuvant and Freund's Incomplete Adjuvant, mycolate-based adjuvants (*e.g.*, trehalose dimycolate), bacterial lipopolysaccharide (LPS), peptidoglycans (*i.e.*, mureins, mucopeptides, or glycoproteins such as N-Opaca, muramyl dipeptide [MDP], or MDP analogs), proteoglycans (*e.g.*, extracted from *Klebsiella pneumoniae*), streptococcal preparations (*e.g.*, OK432), Biostim™ (*e.g.*, 01K2), the "Iscoms" of EP 109 942, EP 180 564 and EP 231 039, aluminum hydroxide, saponin, DEAE-dextran, neutral oils (such as miglyol), vegetable oils (such as arachis oil), liposomes, Pluronic® polyols, the Ribi adjuvant system (see, for example GB-A-2 189 141), or interleukins, particularly those that stimulate cell mediated immunity. An alternative adjuvant consisting of extracts of *Amycolata*, a bacterial genus in the order Actinomycetales, has been described in U.S. Patent No. 4,877,612. Additionally, proprietary adjuvant mixtures are commercially available. The adjuvant used will depend, in part, on the

recipient organism. The amount of adjuvant to administer will depend on the type and size of animal. Optimal dosages may be readily determined by routine methods.

The vaccine compositions optionally may include vaccine-compatible pharmaceutically acceptable (*i.e.*, sterile and non-toxic) liquid, semisolid, or solid  
5 diluents that serve as pharmaceutical vehicles, excipients, or media. Any diluent known in the art may be used. Exemplary diluents include, but are not limited to, polyoxyethylene sorbitan monolaurate, magnesium stearate, methyl- and propylhydroxybenzoate, talc, alginates, starches, lactose, sucrose, dextrose, sorbitol, mannitol, gum acacia, calcium phosphate, mineral oil, cocoa butter, and oil of  
10 theobroma.

The vaccine compositions can be packaged in forms convenient for delivery. The compositions can be enclosed within a capsule, caplet, sachet, cachet, gelatin, paper, or other container. These delivery forms are preferred when compatible with entry of the immunogenic composition into the recipient organism  
15 and, particularly, when the immunogenic composition is being delivered in unit dose form. The dosage units can be packaged, *e.g.*, in tablets, capsules, suppositories or cachets.

The vaccine compositions may be introduced into the subject to be immunized by any conventional method including, *e.g.*, by intravenous, intradermal,  
20 intramuscular, intramammary, intraperitoneal, or subcutaneous injection; by oral, sublingual, nasal, anal, or vaginal, delivery. The treatment may consist of a single dose or a plurality of doses over a period of time.

The invention also comprehends use of an attenuated bacterial strain of the invention for manufacture of a vaccine medicament to prevent or alleviate  
25 bacterial infection and/or symptoms associated therewith. The invention also provides use of inhibitors of the invention for manufacture of a medicament to prevent or alleviate bacterial infection and/or symptoms associated therewith.

The present invention is illustrated by the following examples.  
Example 1 describes constructions of *P. multocida* mutants. Example 2 relates to  
30 screening for *P. multocida* mutants. Example 3 addresses methods to determine

virulence of the *P. multocida* mutants. Example 4 describes cloning of *P. multocida* virulence genes. Example 5 addresses identification of genes in other species related to *P. multocida* virulence genes. Example 6 describes construction of *A. pleuropneumoniae* mutants. Example 7 addresses screening for attenuated *A. pleuropneumoniae* mutants. Example 8 relates to identification of *A. pleuropneumoniae* virulence genes. Example 9 describes competition challenge of *A. pleuropneumoniae* mutants and wild type bacteria. Example 10 characterizes *A. pleuropneumoniae* genes identified. Example 11 addresses efficacy of *A. pleuropneumoniae* mutant to protect against wild type bacterial challenge. Example 12 describes identification of species homolog virulence genes in *P. (Mannheimia) haemolytica*.

#### Example 1

##### Construction of a Library of Tagged-Transposon *P. multocida* Mutants

A library of tagged-transposon mutants was constructed in parental vector pLOF/Km [Herrero, *et al.*, *J Bacteriol.* 172:6557-67 (1990)] which has previously been demonstrated to be functional and random in *P. multocida* [Lee, *et al.*, *Vet Microbiol.* 50:143-8 (1996)]. Plasmid pLOF/Km was constructed as a modification of suicide vector pGP704 and included a transposase gene under control of the *Tac* promoter as well as the mini-Tn10 transposable element encoding kanamycin resistance. Plasmid pTEF-1 was constructed as described below by modifying pLOF/Km to accept sequence tags which contained a semi-random [NK]<sub>35</sub> sequence.

Plasmid pLOF/Km was first modified to eliminate the unique *KpnI* restriction site in the multiple cloning region and then to introduce a new *KpnI* site in the mini-Tn10 region. The plasmid was digested with *KpnI* and the resulting overhanging ends were filled in with Klenow polymerase according to manufacturer's suggested protocol. Restriction digests and ligations described herein were performed according to manufacturer's suggested protocols (Gibco BRL, Gaithersburg, MD and Boehringer Mannheim, Indianapolis, IN). The blunt end product was self-ligated to

produce a plasmid designated pLOF/Km--*KpnI* which was transformed into *E.coli* DH5 $\alpha$ : $\lambda$ pir for amplification. *E.coli* DH5 $\alpha$ : ( $\lambda$ pir  $\phi$ 80dlacZ $\Delta$ M15, recA1, endA1, gyrA96, thi-1, hsdR17(r<sub>k</sub><sup>-</sup>, m<sub>k</sub><sup>-</sup>, supE44, relA1, deoR,  $\Delta$ (lacZYA-argF)U169, was propagated at 37°C in Luria-Bertani (LB) medium. Plasmids were prepared using

5 QIAGEN SpinPreps from QIAGEN Inc. (Santa Clarita, CA) and digested with *SfiI* which cuts at a unique site within the mini-Tn10 transposable element. A *SfiI*-*KpnI*-*SfiI* adaptor was prepared by annealing oligonucleotides TEF1 (SEQ ID NO: 86) and TEF3 (SEQ ID NO: 87) and the resulting double-stranded adapter was ligated into the *SfiI* site to create plasmid pTEF-1. Oligonucleotides TEF1 and TEF3 (as well as all

10 other oligonucleotides described herein) were synthesized by Genosys Biotechnologies (The Woodlands, TX).

TEF1 5'-AGGCCGGTACCGGCCGCCT SEQ ID NO: 86

15 TEF3 5'-CGGCCGGTACCGGCCTAGG SEQ ID NO: 87

Unique sequence tags for insertion into the *KpnI* site of pTEF-1 were prepared as follows. PCR was carried out to generate double stranded DNA tags using a GeneAmp XL PCR Kit (PE Applied Biosystems, Foster City, CA) under

20 conditions including 250  $\mu$ M each dNTP, 1.5 mM Mg(OAc)<sub>2</sub>, 100 pmol each primer TEF14 (SEQ ID NO: 88) and TEF15 (SEQ ID NO: 89), 1 ng TEF26 (SEQ ID NO: 90) as template DNA and 2.5 units recombinant *Tth* DNA Polymerase XL.

TEF14 5'-CATGGTACCCATTCTAAC SEQ ID NO: 88

25

TEF15 5'-CTAGGTACCTACAACCTC SEQ ID NO: 89

TEF26 SEQ ID NO: 90

5'-CTAGGTACCTACAACCTCAAGCTT-[NK]<sub>35</sub>-

30

AAGCTTGGTTAGAATGGGTACCATG

Reaction conditions included an initial incubation at 95°C for one minute, followed by thirty cycles of 30 seconds at 95°C, 45 seconds at 45°C, and 15 seconds at 72°C, followed by a final incubation at 72°C for two minutes. The PCR products were digested with *KpnI* and purified using a QIAGEN Nucleotide Removal Kit (QIAGEN, Inc., Chatsworth, GA) according to the manufacturer's suggested protocol. The unique tag sequences were ligated into the mini-Tn10 element of linearized pTEF-1, previously digested with *KpnI* and dephosphorylated with calf intestinal alkaline phosphatase (Boehringer Mannheim) using standard procedures. The resulting plasmid library was transformed into *E.coli* DH5 $\alpha$ : $\lambda$ pir. Colony blot analysis was performed according to the DIG User's Guide (Boehringer-Mannheim) with hybridization and detection performed as follows.

Hybridizations were essentially performed according to the Genius Non-Radioactive User's Guide (Boehringer Mannheim Biochemicals), the product sheet for the DIG-PCR labeling kit (Boehringer Mannheim Biochemicals), and the product sheet for CSPD (Boehringer Mannheim Biochemicals). For preparation of probes, a 100  $\mu$ l primary PCR reaction was set up using Amplitaq PCR buffer (PE Applied Biosystems), 200  $\mu$ M dNTPs, 140 pmol each of primers TEF5 (SEQ ID NO: 91) and TEF6 (SEQ ID NO: 92), 2 mM MgCl<sub>2</sub>, 2.5 units Amplitaq (PE Applied Biosystems) and 1 ng of plasmid DNA.

20

TEF5      5'-TACCTACAACCTCAAGCT      SEQ ID NO: 91

TEF6      5'-TACCCATTCTAACCAAGC      SEQ ID NO: 92

Cycle conditions included an initial incubation at 95°C for two minutes, followed by 35 cycles of 95°C for 30 seconds, 50°C for 45 seconds, 72°C for 15 seconds and a final incubation at 72°C for three minutes. The amplification products were separated using electrophoresis on a 2% - 3:1 NuSieve GTG (FMC BioProducts, Rockland, ME, USA):Agarose gel and the 109 bp product was excised and purified. Gel extractions were carried out using a QIAGEN Gel Extraction kit (QIAGEN).

30



Approximately 15 ng of the primary product was labeled in a 50 µl PCR reaction using the DIG PCR Kit, 50 pmol each of primers TEF24 and TEF25, and a 1:1 mix of DIG Probe Synthesis Mix with 2 mM dNTP stock solution.

5                      TEF24        5'-TACCTACAACCTCAAGCTT        SEQ ID NO: 93

                         TEF25        5'-TACCCATTCTAACCAAGCTT        SEQ ID NO: 94

10                      PCR conditions included an initial incubation at 95°C for four minutes, followed by 25 cycles of 95°C for 30 seconds, 50°C for 45 seconds, 72°C for 15 seconds and a final incubation at 72°C for three minutes. The labeled PCR product was digested with *HindIII* in a total reaction volume of 90 µl and purified from the constant primer arms using a 2% - 3:1 NuSieve GTG (FMC BioProducts):Agarose gel. The region containing the labeled variable tag was excised and the entire gel slice was dissolved and denatured in 10 ml of DIG EasyHyb at 95°C for ten minutes.

15                      Dot blots were prepared using a Hybond<sup>®</sup>-N<sup>+</sup> membrane (Amersham-Pharmacia Biotech). Target DNA for each tag was prepared in 96 well plates using approximately 30 ng of PCR product. An equal volume of 0.1 N NaOH was added to denature the sample and each sample was applied to the membrane with minimal vacuum using a Minifold I<sup>™</sup> Dot-Blot Apparatus from Schleicher and Schuell (Keene, NH, USA). Each well was washed with 150 µl of Neutralization Solution (0.5 M Tris /3 M NaCl, pH 7.5) and 150 µl of 2X SSC. Membranes were UV-crosslinked in a Stratalinker (Stratagene, La Jolla, CA, USA) and prehybridized for one hour in 20 mls DIG EasyHyb Buffer at 42°C. The denatured probe was added and hybridization carried out overnight at 42°C. The membrane was washed two times in 2X SSC containing 0.1% SDS for five minutes each wash. Two high stringency washes were performed in 50 ml of pre-warmed 0.1X SSC buffer containing 0.1% SDS at 68°C for 15 minutes before proceeding with standard Genius Detection protocols (Genius Manual ).

20

25

It is desirable to use a non-radioactive detection system for safety, lower cost, ease of use, and reduction of hazardous materials. In initial experiments using similar procedures previously described [Mei, *et al.*, *Mol Microbiol.* 26:399-407 (1997)], unacceptable background levels of hybridization were obtained in  
5 negative controls. In order to decrease background, tag length was increased by 30 bp to a total of 70, amplification primers were lengthened to include all sequence flanking the variable region, a lower concentration of dig-dUTP was used, and the conserved sequences flanking the sequence tag region were removed by gel purification. Most significantly, PCR was used to generate [NK]<sub>35</sub> sequence tags as  
10 the target DNA in dot blots rather than the entire plasmids containing the tagged transposons after detecting background hybridization from the transposon itself. Using these modifications background was eliminated making chemiluminescent/non-radioactive screening more effective.

Approximately four hundred different transformants resulting from the  
15 ligation of pTEF-1 with the PCR generated sequence tags were screened by colony blot and the 96 strongest hybridizing colonies were assembled into microtiter plates for further use. Even though the likelihood of duplicated tags was very low, half of the plate of master tags was probed against the other to confirm that no tags were duplicated. The plasmids containing these tags were purified and transformed into  
20 *E.coli* S17-1:λpir (pir, *recA*, *thi*, *pro*, *hsd*, (r-m+), RP4-2, (Tc::Mu), (Km::Tn7), [TmpR], [SmR]), and the transformed bacteria propagated at 37°C in Luria-Bertani (LB) medium. Each of the 96 *E.coli* S17-1:λpir transformants containing the tagged plasmid pTEF-1 was used in conjugative matings to generate transposon mutants of *P. multocida*. *P. multocida* strain TF5 is a spontaneous nalidixic acid resistant mutant  
25 derived from UC6731, a bovine clinical isolate. *P. multocida* strains were grown on brain heart infusion (BHI) media (Difco Laboratories, Detroit, MI, USA) at 37°C and in 5% CO<sub>2</sub> when grown on plates. Matings were set up by growing each *E.coli* S17-1:λpir /pTEF1:[NK]<sub>35</sub> clone and the TF5 strain to late log phase. Fifty μl of culture for each tagged-pTEF-1 clone was mixed with 200 μl of the TF5 culture and 50 μl of  
30 each mating mixture was spotted onto 0.22 TM filters previously placed on BHI plates

containing 100 mM IPTG and 10 mM MgSO<sub>4</sub>. Following overnight incubation at 37°C with 5% CO<sub>2</sub>, mating mixtures were washed off of each filter into 3 ml of PBS and 25 µl of each was plated onto BHIN<sup>50</sup>K<sup>100</sup> plates. Following selective overnight growth, colonies were assembled into microtiter plates by toothpick transfer into 200 µl BHIN<sup>50</sup>K<sup>50</sup> making sure that each well in a microtiter plate always contained a transposon mutant with the same sequence tag. Following overnight growth, 50 µl of 75% glycerol was added to each well and plates were stored frozen at -80°C.

Nineteen pools were assembled by transferring the transposon mutants to microtiter plates making sure that each well contained a transposon mutant with the appropriate tag for that well. In other words, a specific well in each microtiter plate always contained a transposon mutant with the same sequence tag even though the location of the transposon within those mutants may be different.

## **Example 2**

### **Murine Screening for Attenuated *P. multocida* Mutants**

Nineteen pools of *Pasteurella multocida* transposon mutants were screened using a murine model of septicemia. Frozen plates of pooled *P. multocida* transposon mutants were removed from -80°C storage and subcultured by transferring 10 µl from each well to a new 96 well round bottom plate (Corning Costar, Cambridge, MA, USA) containing 200 µl of brain heart infusion (DIFCO) with 50 µg/ml nalidixic acid (Sigma) and 50 µg/ml kanamycin (Sigma) (BHIN<sup>50</sup>K<sup>50</sup>). Plates were incubated without shaking overnight at 37°C in 5% CO<sub>2</sub>. Overnight plates were subcultured by transferring 10 µl from each well to a new flat bottomed 96-well plate (Corning Costar) containing 100 µl of BHI per well and incubating at 37°C with shaking at approximately 150 rpm. The OD<sub>540</sub> was monitored using a micro-titer plate reader. At an OD<sub>540</sub> of approximately 0.2 to 0.25, each plate was pooled to form the "input pool" by combining 100 µl from each of the wells of the micro-titer plate. The culture was diluted appropriately in BHI to doses of approximately 10<sup>4</sup>, 10<sup>5</sup>, 10<sup>6</sup> CFU/ml and 0.2 ml of each dilution was used to infect female 14-16 g BALB/c mice by intraperitoneal administration. At two days post-infection, one or two surviving mice were euthanized and the spleens harvested. The entire spleen was homogenized

in 1.0 ml sterile 0.9 % saline. Dilutions of the homogenate from  $10^{-2}$  to  $10^{-5}$  were prepared and plated onto BHIN<sup>50</sup>K<sup>50</sup> plates. Following overnight growth, at least 20,000 colonies were pooled in 10 mls BHI broth to form the "recovered pool" and 0.5 ml of the recovered pool was centrifuged at 3,500 X g and the pellet used to  
5 prepare genomic DNA according to a previously described protocol [Wilson, *In* F. M. Ausubel, *et al.*, (ed.), Current Protocols in Molecular Biology, vol. 1. John Wiley and Sons, New York, p. 2.4.1-2.4.5. (1997)].

Initial experiments with virulent wild-type *P. multocida* indicated that organisms could be recovered from the spleen, lungs, kidneys, and liver indicating a  
10 truly septicemic model of infection. Dot blots for both the "input" and "recovered" pools were performed as described in Example 1 and evaluated both by visual inspection and by semi-quantitative analysis. Hybridization was carried out as described in Example 1 except that 5 µg of genomic DNA from input and recovered pools was used as template. Semi-quantitative analysis indicates whether a significant  
15 reduction in a single clone has occurred. If a mutant is unable to survive within the host, then the recovered signal should be very low compared to the input signal yielding a high input/recovered ratio. Most mutants will grow as well *in vivo* as *in vitro* and therefore a ratio of their signals should be approximately equal to 1. Clones selected by quantitative analysis as being highly reduced in the recovered pool were  
20 selected for further study. Additional clones with questionable input/recovered ratios were also selected after visually evaluating films made from the dot blots.

### Example 3 Determination of Virulence for *P. multocida* Candidate Mutants

25 Each potential mutant which exhibited reduced recovery from splenic tissue was isolated from the original pool plate and used individually in a challenge experiment to verify and roughly estimate the attenuation caused by the transposon mutation. Individual candidate mutants from *in vivo* screens were grown on Sheep Blood Agar plates overnight in 5% CO<sub>2</sub> at 37°C. Approximately six colonies of each  
30 mutant were inoculated into BHI broth and allowed to grow for six hours. Dilutions were prepared and five mice each were infected as described above with  $10^2$ ,  $10^3$ ,  $10^4$

and  $10^5$  CFU each. Attenuation was determined by comparing mortality after six days relative to the wild type. Surviving mice were presumed to be protected and then challenged with a dose of wild type *P. multocida* at a concentration approximately 200-fold greater than the  $LD_{50}$  for the wild type strain. Survival rate was then determined for each challenged group of mice.

Results indicated that 62 of 120 potential transposon mutants were attenuated, having an approximate  $LD_{50}$  of at least 10 fold higher than the wild type strain. The clones and their approximate  $LD_{50}$  values are listed in Table 1. A control experiment with the wild type strain was run in parallel with each set of challenges and in all cases mortality in wild type-challenged groups was 100%.

In addition to  $LD_{50}$  values, Table 1 also provides data from vaccination and challenge experiments. Briefly, groups of mice ( $n = 5$  to 10) were vaccinated by intraperitoneal injection with the individual *P. multocida* strains shown in Table 1 at a dose that was approximately 200 times greater than the  $LD_{50}$  of the virulent, wild type strain. Animals were observed for 28 days after which mortality figures were calculated.

**Table 1**  
***P. multocida* Virulence Genes**

Nucleotide SEQ ID NO:	Representative Isolate	Possible Gene Function	Vaccination # survivors/total	Challenge # survivors/total	$LD_{50}$
—	wild type	-	0/10	-	<10
23	PM1B1	guaB	10/10, 10/10, 10/10	9/10, 9/10	$4.3 \times 10^6$
11	PM1D1	dsbB	10/10, 5/10	10/10, 5/5	$8.4 \times 10^4$
3	PM1BD7	atpG	5/5, 10/10	10/10	$>3 \times 10^5$
74	PM1BE11	yhjC (HI0145)	10/10	5/10	$>2 \times 10^5$
70	PM1BF6	yabK (HI1020)	3/5, 8/10	9/9	$>2 \times 10^5$
19	PM2G8	fhaC	4/5, 9/10	9/9	$>4 \times 10^5$
76	PM3C9	yiaO (HI0146)	3/5		$>6 \times 10^5$
118	PM3G11	UnkO	4/5, 10/10	10/10	$>3 \times 10^5$
31	PM7B4	iroA (UnkB)	0/5		
17	PM4C6	fhaB (fhaB2)	2/5, 10/10, 9/10	10/10, 9/9	$>3 \times 10^6$
9	PM4G10-T9	dnaA	4/5		$>5 \times 10^5$
1	PM4D5-T5	atpB	5/5		$>4 \times 10^5$
53	PM4D5-T1	UnkC2	5/5		$>4 \times 10^5$
15	PM4F2	fhaB (fhaB1)	3/5, 6/10, 10/10	6/6, 10/10	$>3 \times 10^5$
41	PM5F7	mreB	4/5		$1 \times 10^3$
7	PM5E2	devB	0/5, 3/10	2/3	ND
68	PM6H5-T1	xylA	5/5		$>3 \times 10^5$
78	PM6H8	yigF (HI0719)	5/5, 9/10	9/9	$>3 \times 10^5$
108	PM7D12	pnp	5/5, 9/10	9/9	
51	PM8C1R1-T2	UnkC1	5/5		$\sim 6 \times 10^5$

Nucleotide SEQ ID NO:	Representative Isolate	Possible Gene Function	Vaccination # survivors/total	Challenge # survivors/total	LD <sub>50</sub>
37	PM8C1-T3	mgIB	5/5		-6 x 10 <sup>5</sup>
58	PM8C1R1-T6	UnkD1	5/5		-6 x 10 <sup>5</sup>
45	PM10H7	purF (HI1707)	3/5, 8/10, 8/10	8/8, 8/8	>3 x 10 <sup>5</sup>
25	PM10H10-T2	HI1501	5/5		>1 x 10 <sup>4</sup>
72	PM11G8-T2	ygiK	5/5		>2.4 x 10 <sup>3</sup>
21	PM11G8-T4	greA	5/5		>2.4 x 10 <sup>3</sup>
84	PM12H6	yyam (HI0687)	3/5, 0/10		-2.2 x 10 <sup>3</sup>
33	PM15G8-T2	kdtB	5/5		>1.2 x 10 <sup>5</sup>
116	PM15G8-T1	UnkK	5/5		>1.2 x 10 <sup>5</sup>
104	PM16G11-T1	hmbR	3/5		>1.9 x 10 <sup>5</sup>
29	PM16G11-T2	hxuC	3/5		>1.9 x 10 <sup>5</sup>
35	PM16H8	lgtC	5/5, 10/10	10/10	>2.4 x 10 <sup>5</sup>
80	PM16H3	yleA (HI0019)	5/5, 10/10		>2.0 x 10 <sup>5</sup>
49	PM17H6-T1	sopE	4/5		-6 x 10 <sup>5</sup>
120	PM17H6	UnkP	4/5		-6 x 10 <sup>5</sup>
5	PM18F5-T8	cap5E	5/5		>2.4 x 10 <sup>5</sup>
82	PM18F5-T10	yojB (HI0345)	5/5		>2.4 x 10 <sup>5</sup>
13	PM19A1	exbB	5/5, 10/10	10/10	>1.2 x 10 <sup>5</sup>
112	PM19D4	rci	5/5, 8/10	8/8	-1.6 x 10 <sup>5</sup>
39	PM20A12	mioC (HI0669)	3/5, 8/10	8/8	-2 x 10 <sup>4</sup>
60	PM20C2	UnkD2	5/5, 10/10	10/10	>8.2 x 10 <sup>6</sup>

#### Example 4 Cloning and Identification of Genes Required for *P. multocida* Virulence

Each transposon mutant which was verified to be attenuated was analyzed further to determine the identity of the disrupted open reading frame. DNA from each mutant was amplified, purified, and digested with restriction enzymes that were known not to cut within the transposon and generally produced 4-8 kb fragments that hybridized with the transposon. Using selection for kanamycin resistance encoded by the transposon, at least one fragment for each transposon mutant was cloned.

Southern hybridization with multiple restriction enzymes was performed for each attenuated mutant using a labeled 1.8 kb *Mlu*I fragment from pLOF/Km as a probe to identify a suitably sized fragment for cloning. The mini-Tn10 element and flanking DNA from each mutant was cloned into pUC19 and the flanking sequence determined using internal primers TEF32 and TEF40, primer walking and in some cases universal pUC-19 primers.

TEF-32      GGCAGAGCATTACGCTGAC      SEQ ID NO: 95  
 TEF-40      GTACCGGCCAGGCGGCCACGCGTATTC      SEQ ID NO:96

Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry  
 5 kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377  
 DNA Sequencer. Double stranded sequence for putative interrupted open reading  
 frames was obtained for each clone. Sequencer 3.0 software (Genecodes, Corp., Ann  
 Arbor, MI) was used to assemble and analyze sequence data. GCG programs  
 [Devereux, *et al.*, 1997. Wisconsin Package Version 9.0, 9.0 ed. Genetics Computer  
 10 Group, Inc., Madison] were used to search for homologous sequences in currently  
 available databases.

In 37% of the clones that were identified as being attenuated, there  
 were multiple insertions of the mini-Tn10 transposable element. Each insertion  
 including its flanking sequence was cloned individually into pGP704 and mated into  
 15 the wild-type strain to produce new mutants of *P. multocida*, each carrying only one  
 of the multiple original insertions. Individual mutants were retested individually to  
 determine the insertion responsible for the attenuated phenotype. The nucleotide  
 sequence of the disrupted, predicted open reading frame was determined by  
 sequencing both strands, and the predicted amino acid sequence was used to search  
 20 currently available databases for similar sequences. Sequences either matched known  
 genes, unknown genes, and hypothetical open reading frames previously sequenced or  
 did not match any previously identified sequence. For those genes having homology  
 to previously identified sequences, potential functions were assigned as set out in  
 Table 1.

25

#### Example 5 Identification of Related Genes in Other Species

In separate experiments, STM was also performed using *Actinobacillus*  
*pleuropneumoniae* (App). One of the App strains contained an insertion in a gene that  
 30 was sequenced (SEQ ID NO: 97) and identified as a species homolog of the *P.*  
*multocida* atpG gene. This result suggested the presence in other bacterial species of

homologs to previously unknown *P. multocida* genes that can also be mutated to produce attenuated strains of the other bacterial species for use in vaccine compositions. In order to determine if homologs of other *P. multocida* genes exists in other bacterial species, Southern hybridization was performed on genomic DNA from other species using the *A. pleuropneumoniae atpG* gene as a probe.

*Actinobacillus pleuropneumoniae*, *Pasteurella haemolytica* (Ph), *P. multocida*, and *Haemophilus somnus* (Hs) genomic DNA was isolated using the CTAB method and digested with *EcoRI* and *HindIII* for two hours at 37°C. Digested DNA was separated on a 0.7% agarose gel at 40V in TAE buffer overnight. The gel was immersed sequentially in 0.1 M HCL for 30 minutes, twice in 0.5 M NaOH/1.5 M NaCl for 15 minutes each, and twice in 2.5 M NaCl/1 M Tris, pH 7.5. The DNA was transferred to nitrocellulose membranes (Amersham Hybond N<sup>+</sup>) overnight using 20X SSC buffer (3 M NaCl/0.3 M sodium citrate). The DNA was crosslinked to the membrane using a UV Stratalinker on autocrosslink setting (120 millijoules). The membrane was prehybridized in 5X SSC/ 1% blocking solution/0.1% sodium lauroyl sarcosine/0.02% SDS at 50°C for approximately seven hours and hybridized overnight at 50°C in the same solution containing a PCR generated atpG probe.

The probe was prepared using primers DEL-1389 (SEQ ID NO: 98) and TEF-46 (SEQ ID NO: 99) in a with a GeneAmp XL PCR kit in a GeneAmp PCR System 2400. Template was genomic *A. pleuropneumoniae* DNA.

DEL-1389	TCTCCATTCCCTTGCTGCGGCAGGG	SEQ ID NO: 98
TEF-46	GGAATTACAGCCGGATCCGGG	SEQ ID NO: 99

The PCR was performed with an initial heating step at 94°C for five minutes, 30 cycles of denaturation t 94°C for 30 sec, annealing at 50°C for 30 sec, and elongation at 72°C for three minutes, and a final extension step at 72°C for five minutes. The amplification products were separated on an agarose gel, purified using a QIAquick gel purification kit (QIAGEN), and labeled using a DIG-High Primer kit (Boehringer Mannheim). The blot was removed from the hybridization solution and rinsed in 2X



SSC and washed two times for five minutes each wash in the same buffer. The blot was then washed two times for 15 minutes each in 0.5X SSC at 60°C. Homologous bands were visualized using a DIG Nucleic Acid Detection Kit (Boehringer Mannheim).

5 Single bands were detected in *Pasteurella haemolytica*, *Haemophilus somnus* and *A. pleuropneumoniae* using *EcoRI* digested DNA. Two bands were detected using *EcoRI* digested DNA from *Pasteurella multocida*.

### Example 6

#### 10 Construction of a Library of Tagged-Transposon *P. multocida* Mutants

Transposon mutagenesis using pLOF/Km has previously been reported to be functional and random in *A. pleuropneumoniae* [Tascon, *et al.*, *J Bacteriol.* 175:5717-22 (1993)]. To construct tagged transposon mutants of *A. pleuropneumoniae*, each of 96 *E. coli* S17-1: $\lambda$ pir transformants containing pre-  
 15 selected tagged plasmids (pTEF-1:[NK]<sub>35</sub>) was used in conjugative matings to generate transposon mutants of *A. pleuropneumoniae* strain AP225, a serotype 1 spontaneous nalidixic acid resistant mutant derived from an in vivo passaged ATCC 27088 strain. *A. pleuropneumoniae* strains were grown on Brain Heart Infusion (BHI) (Difco Laboratories, Detroit, MI) media with 10  $\mu$ g/ml B-nicotinamide adenine  
 20 dinucleotide (V<sup>10</sup>), (Sigma, St. Louis, Missouri) at 37°C and in 5% CO<sub>2</sub> when grown on plates. *E. coli* S17-1: $\lambda$ pir ( $\lambda$ pir, *recA*, *thi*, *pro*, *hsdR*(r<sub>k</sub><sup>-</sup>,m<sub>k</sub><sup>+</sup>), RP4-2, (Tc<sup>R</sup>::Mu), (Km<sup>R</sup>::Tn7), [Tnp<sup>R</sup>], [Sm<sup>R</sup>]) was propagated at 37°C in Luria-Bertani (LB) medium. Antibiotics when necessary were used at 100  $\mu$ g/ml ampicillin (Sigma), 50  $\mu$ g/ml nalidixic acid (N<sup>50</sup>)(Sigma), and 50 (K<sup>50</sup>) or 100 (K<sup>100</sup>)  $\mu$ g/ml of kanamycin (Sigma).

25 Matings were set up by growing each *E. coli* S17-1: $\lambda$ pir/pTEF1:[NK]<sub>35</sub> clone and the AP225 strain to late log phase. A 50  $\mu$ l aliquot of culture for each tagged-pTEF-1 clone was mixed with 150  $\mu$ l of the APP225 culture, and then 50  $\mu$ l of each mating mixture was spotted onto 0.22  $\mu$ M filters previously placed onto BHIV<sup>10</sup> plates containing 100  $\mu$ M IPTG and 10 mM MgSO<sub>4</sub>. Following overnight incubation  
 30 at 37°C with 5% CO<sub>2</sub>, mating mixtures were washed off of each filter into 2 ml of PBS and 200  $\mu$ l of each was plated onto BHIV<sup>10</sup>N<sup>50</sup>K<sup>100</sup> plates. After selective

overnight growth, colonies were assembled into microtiter plates by toothpick transfer into 200  $\mu$ l BHIV<sup>10</sup>N<sup>50</sup>K<sup>50</sup> making sure that each well in a microtiter plate always contained a transposon mutant with the same sequence tag. Following overnight growth, 50  $\mu$ l of 75% glycerol was added to each well and plates were stored frozen at -80°C.

APP does not appear to have as much bias towards multiple insertions of the mini-Tn10 element as did *P. multocida*. Only approximately 3% of the mutants were determined to contain multiple insertions, which is in agreement with the 4% previously reported [Tascon, *et al.*, *J Bacteriol.* 175:5717-22 (1993)]. A problem in APP consisted of identifying numerous mutants (discussed below) containing insertions into 23S RNA regions: 28 total mutants with insertions into 13 unique sites. This may indicate that 23S RNA contains preferential insertion sites and that the growth of APP is affected by these insertions enough to result in differential survival within the host. Southern blot analysis using an APP 23S RNA probe suggests that APP may contain only three ribosomal operons as compared to five in *H. influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)] and seven complete operons in *E. coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)]. This site preference and its effect on growth rate may be a significant barrier to "saturation mutagenesis" since a significant number of clones will contain insertions into these rRNAs and large volume screening will be necessary to obtain additional unique attenuating mutations.

#### Example 7

##### Porcine Screening for Attenuated *A. pleuropneumoniae* Mutants

Twenty pools of *A. pleuropneumoniae* transposon mutants, containing a total of approximately 800 mutants, were screened using a porcine intratracheal infection model. Each pool was screened in two separate animals.

Frozen plates of pooled *A. pleuropneumoniae* transposon mutants were removed from -80°C storage and subcultured by transferring 20  $\mu$ l from each well to a new 96 well round bottom plate (Corning Costar, Cambridge, MA, USA) containing 180  $\mu$ l of BHIV<sup>10</sup>N<sup>50</sup>K<sup>50</sup>. Plates were incubated without shaking overnight at 37°C in

5% CO<sub>2</sub>. Overnight plates were then subcultured by transferring 10 µl from each well to a new flat bottomed 96 well plate (Corning Costar) containing 100 µl of BHIV<sup>10</sup> per well and incubating at 37°C with shaking at 150 rpm. The OD<sub>562</sub> was monitored using a microtiter plate reader. At an OD<sub>562</sub> of approximately 0.2 to 0.25, each plate was pooled to form the "input pool" by combining 100 µl from each of the wells of the microtiter plate. The culture was diluted appropriately in BHI to approximately 2 X 10<sup>6</sup> CFU/ml. For each diluted pool, 4.0 ml was used to infect 10-20 kg SPF pigs (Whiteshire-Hamroc, Albion, IN) by intratracheal administration using a tracheal tube. At approximately 20 hours post-infection, all surviving animals were euthanized and the lungs removed. Lavage was performed to recover surviving bacteria by infusing 150 mls of sterile PBS into the lungs, which were then massaged to distribute the fluid. The lavage fluid was recovered, and the process was repeated a second time. The lavage fluid was centrifuged at 450 x g for 10 minutes to separate out large debris. Supernatants were then centrifuged at 2,800 x g to pellet the bacteria. Pellets were resuspended in 5 mls BHI and plated in dilutions ranging from 10<sup>-2</sup> to 10<sup>-5</sup> onto BHIV<sup>10</sup>N<sup>50</sup>K<sup>50</sup> plates. Following overnight growth, at least 100,000 colonies were pooled in 10 mls BHI broth to form the "recovered pools". A 0.7 ml portion of each recovered pool was used to prepare genomic DNA by the CTAB method [Wilson, *In* Ausubel, *et al.*, (eds.), Current Protocols in Molecular Biology, vol. 1. John Wiley and Sons, New York, p. 2.4.1-2.4.5 (1997)].

Recovery from the animals routinely was in the 10<sup>8</sup> CFU range from lung lavage.

Dot blots were performed and evaluated both by visual inspection and by semi-quantitative analysis as described previously. All hybridizations and detections were performed as described. Briefly, probes were prepared by a primary PCR amplification, followed by agarose gel purification of the desired product and secondary PCR amplification incorporating dig-dUTP. Oligonucleotides including TEF5, TEF6, TEF24, TEF25, TEF48 and TEF62, were synthesized by Genosys Biotechnologies (The Woodlands, TX). Primers TEF69, TEF65, and TEF66 were also used for inverse PCR reactions and sequencing.

TEF69	GACGTTTCCCGTTGAATATGGCTC	SEQ ID NO: 166
TEF65	GCCGGATCCGGGATCATATGACAAGA	SEQ ID NO: 167
TEF66	GACAAGATGTGTATCCACCTTAAC	SEQ ID NO: 168

5

The labeled PCR product was then digested with *Hind*III to separate the constant primer arms from the unique tag region. The region containing the labeled variable tag was excised and the entire gel slice was then dissolved and denatured in DIG EasyHyb. Dot blots were prepared and detected using the standard CSPD detection protocol. Film exposures were made for visual evaluation, and luminescent counts per second (LCPS) were determined for each dot blot sample. The  $LCPS_{input} / LCPS_{recovered}$  ratio for each mutant was used to determine mutants likely to be attenuated.

Clones selected as being present in the input pool but highly reduced in the recovered pool were selected for further study. Additional clones with questionable input/recovered ratios were also selected after visually evaluating films made from the dot blots. A total of 110 clones were selected.

#### Example 8

##### Identification of *A. pleuropneumoniae* Virulence Genes

A partial flanking sequence was determined for each of the 110 mutants by inverse PCR and direct product sequencing. Inverse PCR was used to generate flanking DNA products for direct sequencing as described above. Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 DNA Sequencer. Sequencher 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs [Devereux and Haeberli, Wisconsin Package Version 9.0, 9.0 ed. Genetics Computer Group, Inc., Madison (1997)] were used to search for homologous sequences in currently available databases.

Table 2 shows the *A. pleuropneumoniae* genes identified and extent to which open reading frames were determinable. Sequence identification numbers are provided for nucleotide sequences as well as deduced amino acid sequences where located.

5

**Table 2**  
***A. pleuropneumoniae* Open Reading Frames**

<u>Complete Open Reading Frame</u>		<u>NO Start Codon - Stop Codon</u>	
10	atpH	SEQ ID NO: 134	dkSA
	aptG	SEQ ID NO: 132	dnaK
	exbB	SEQ ID NO: 140	HI0379
	OmpP5	SEQ ID NO: 152	
15	OmpP5-2	SEQ ID NO: 150	<u>NO Start Codon - NO Stop Codon</u>
	tig	SEQ ID NO: 160	pnp
	fkpA	SEQ ID NO: 142	apvA-or 1
	hupA	SEQ ID NO: 146	apvA-or 2
20	rpmF	SEQ ID NO: 158	apvB
			apvD
<u>Start Codon - NO Stop Codon</u>		<u>RNA or Noncoding Sequences</u>	
20	lpdA	SEQ ID NO: 148	tRNA-leu
	potD	SEQ ID NO: 156	SEQ ID NO: 162
	yaeE	SEQ ID NO: 164	tRNA-glu
	apvC	SEQ ID NO: 128	SEQ ID NO: 163

25

The putative identities listed in Table 3 (below, Example 9) were assigned by comparison with bacterial databases. The 110 mutants represented 35 groups of unique transposon insertions. The number of different mutations per loci varied, with some clones always containing an insertion at a single site within an ORF to clones containing insertions within different sites of the same ORF. Three multiple

30 insertions were detected in the 110 mutants screened as determined by production of multiple PCR bands and generation of multiple sequence electropherograms.

**Example 9**  
**Competition Challenge of *A. pleuropneumoniae***  
**Mutants with Wild Type APP225**

A representative clone from each of the unique attenuated mutant groups identified above that was absent or highly reduced in the recovered population was isolated from the original pool plate and used in a competition challenge experiment with the wild type strain (AP225) to verify the relative attenuation caused by the transposon mutation. Mutant and wild type strains were grown in BHIV<sup>10</sup> to an OD<sub>590</sub> of 0.6 – 0.9. Approximately 5.0 x 10<sup>6</sup> CFU each of the wild type and mutant strains were added to 4 mls BHI. The total 4 ml dose was used infect a 10-20 kg SPF pig by intratracheal administration with a tracheal tube. At approximately 20 hours post-infection, all surviving animals were euthanized and the lungs removed. Lung lavages were performed as described above. Plate counts were carried out on BHIV<sup>10</sup>N<sup>50</sup> and BHIV<sup>10</sup>N<sup>50</sup>K<sup>100</sup> to determine the relative numbers of wild type to mutant in both the input cultures and in the lung lavage samples. A Competitive Index (CI) was calculated as the [mutant CFU / wild type CFU]<sub>input</sub> / [mutant CFU / wild type CFU]<sub>recovered</sub>.

Of the 35 potential transposon mutants, 22 were significantly attenuated, having a competitive index (CI) of less than 0.2. A transposon mutant that did not seem to be attenuated based on the STM screening results was chosen from one of the pools as a positive control. This mutant had a CI in vivo of approximately 0.6. An in vitro competition was also done for this mutant resulting in a CI of 0.8. The mutant was subsequently determined to contain an insertion between 2 phenylalanine tRNA's.

Competitive indices for unique attenuated single-insertion mutants are listed in Table 3. Competitive indices for *atpG*, *pnp*, and *exbB* App mutants indicated that the mutants were unable to compete effectively with the wild type strains and were therefore attenuated.

**Table 3**  
**Virulence and Proposed Function of *A. pleuropneumoniae* Mutants**

	Mutant	Similarity	Putative or Known Functions	C.I.
5	AP20A6	<i>atpH</i>	ATP synthase	.009
	AP7F10	<i>atpG</i>	ATP synthase	.013
	AP17C6	<i>lpdA</i>	dihydrolipoamide dehydrogenase	.039
	AP11E7	<i>exbB</i>	transport of iron compounds	.003,.003,.006
10	AP3H7	<i>potD</i>	Spermidine/putrescine transport	.308
	AP8H6	<i>OmpP5</i>	Adhesin / OmpA homolog	.184
	AP18H8	<i>OmpP5-2</i>	Adhesin / OmpA homolog	.552
	AP13E9	<i>tig</i>	Peptidyl-prolyl isomerase	.050
	AP13C2	<i>fkpA</i>	Peptidyl-prolyl isomerase	<.001
15				
	AP15C11	<i>pnp</i>	Polynucleotide phosphorylase	.032
	AP18F12	<i>hupA</i>	Histone – like protein	.001
	AP20F8	<i>dksA</i>	Dosage dependent suppressor of <i>dnaK</i> mutations	.075
	AP5G4	<i>dnaK</i>	Heat shock protein – molecular chaperone	.376
20				
	AP17C9	<i>tRNA-leu</i>	Protein Synthesis	.059
	AP5D6	<i>tRNA-glu</i>	Protein Synthesis	.055
	AP18B2	<i>rpmF</i>	Protein Synthesis	.112
25	AP10E7	<i>yaeA</i>	Unknown	.001
	AP19A5	HI0379	Unknown	.061
	AP10C10	<i>apvA</i>	Unknown	.157
	AP18F5	<i>apvB</i>	Unknown	.103
	AP2A6	<i>apvC</i>	Unknown	.091
30	AP2C11	<i>apvD</i>	Unknown	.014

Accuracy of the CI appeared to be very good as the *exbB* mutant was competed within three different animals yielding CI's of 0.003, 0.003 and 0.006. The use of a Competitive Index number to assign attenuation based upon one competition in a large animal study was further confirmed based on preliminary vaccination results in pigs with 7 mutants (n=8) described below in Example 11.

### Example 10

#### Characterization of Attenuated *A. pleuropneumoniae* Virulence Genes

The *A. pleuropneumoniae* genes identified represent four broad functional classes: biosynthetic enzymes, cellular transport components, cellular regulation components and unknowns.

The *atpG* gene, encoding the F<sub>1</sub>- $\gamma$  subunit of the F<sub>0</sub>F<sub>1</sub> H<sup>+</sup>-ATPase complex, can function in production of ATP or in the transport of protons by hydrolyzing ATP. A related *atpG* attenuated mutant was also identified in *P. multocida*. Another *atp* gene, *atpH*, that encodes the F<sub>1</sub>  $\delta$  subunit was also identified. Phenotypes of *atp* mutants include non-adaptable acid-sensitivity phenotype [Foster, *J Bacteriol.* 173:6896-6902 (1991)], loss of virulence in *Salmonella typhimurium* [Garcia del Portillo, *et al.*, *Infect Immun.* 61:4489-4492 (1993)] and *P. multocida* (above) and a reduction in both transformation frequencies and induction of competence regulatory genes in *Haemophilus influenzae* Rd [Gwinn, *et al.*, *J Bacteriol.* 179:7315-20 (1997)].

LpdA is a dihydrolipoamide dehydrogenase that is a component of two enzymatic complexes: pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase. While the relationship to virulence is unknown, production of LpdA is induced in *Salmonella typhimurium* when exposed to a bactericidal protein from human which may suggest that this induction may be involved in attempts to repair the outer membrane [Qi, *et al.*, *Mol Microbiol.* 17:523-31 (1995)].

Transport of scarce compounds necessary for growth and survival are critical in vivo. ExbB is a part of the TonB transport complex [Hantke, and Zimmerman, *Microbiology Letters.* 49:31-35 (1981)], interacting with TonB in at least two distinct ways [Karlsson, *et al.*, *Mol Microbiol.* 8:389-96 (1993), Karlsson, *et al.*, *Mol Microbiol.* 8:379-88 (1993)]. Iron acquisition is essential for pathogens. In this work, attenuated *exbB* mutants in both APP and *P. multocida* have been identified. Several TonB-dependent iron receptors have been identified in other bacteria [Biswas, *et al.*, *Mol. Microbiol.* 24:169-179 (1997), Braun, *FEMS Microbiol Rev.* 16:295-307 (1995), Elkins, *et al.*, *Infect Immun.* 66:151-160 (1998), Occhino, *et*



*al.*, *Mol Microbiol.* 29:1493-507 (1998), Stojiljkovic and Srinivasan, *J Bacteriol.* 179:805-12 (1997)]. *A. pleuropneumoniae* produces 2 transferrin-binding proteins, which likely depend on the ExbB/ExbD/TonB system, for acquisition of iron. PotD is a periplasmic binding protein that is required for spermidine (a polyamine) transport [Kashiwagi, *et al.*, *J Biol Chem.* 268:19358-63 (1993)]. Another member of the *Pasteurellaceae* family, *Pasteurella haemolytica*, contains a homologue of *potD* (Lpp38) that is a major immunogen in convalescent or outer membrane protein vaccinated calves [Pandher and Murphy, *Vet Microbiol.* 51:331-41 (1996)]. In *P. haemolytica*, PotD appeared to be associated with both the inner and outer membranes. The role of PotD in virulence or in relationship to protective antibodies is unknown although previous work has shown *potD* mutants of *Streptococcus pneumoniae* to be attenuated [Polissi, *et al.*, *Infect. Immun.* 66:5620-9 (1998)].

Relatively few "classical virulence factors," such as adhesins or toxins with the exception of homologues to OMP P5 of *Haemophilus influenzae*, were identified. *H. influenzae* OMP P5 is a major outer membrane protein that is related to the OmpA porin family of proteins [Munson, *et al.*, *M Infect Immun.* 61:4017-20 (1993)]. OMP P5 in nontypeable *Haemophilus influenzae* has been shown to encode a fimbrial subunit protein expressed as a filamentous structure [Sirakova, *et al.*, *Infect Immun.* 62:2002-20 (1994)] that contributes to virulence and binding of both mucin and epithelial cells [Miyamoto and Bakaletz, *Microb Pathog.* 21:343-56 (1996), Reddy, *et al.*, *Infect Immun.* 64:1477-9 (1996), Sirakova, *et al.*, *Infect Immun.* 62:2002-20 (1994)]. A significant finding was identification of two distinct ORF's that appear to encode OMP P5 homologues. This is also the case with two very similar proteins, MOMP and OmpA2 from *Haemophilus ducreyi*. It remains to be determined whether both are functionally involved in the production of fimbriae and whether the presence of two such ORFs represents a divergent duplication with redundant or complementing functions. Interestingly, the two OMP P5 mutants seem to have disparate CI values, suggesting a difference in essentiality or functionality for only one copy. OMP P5 has been shown to undergo molecular variation during chronic infections [Duim, *et al.*, *Infect Immun.* 65:1351-1356 (1997)], however, this

appears to be restricted to a single gene undergoing point mutations resulting in amino acid changes rather than "type switching" due to differential expression of multiple genes.

Protein folding enzymes are important accessories for the efficient  
5 folding of periplasmic and extracellular proteins, and two genes were identified whose products have peptidyl-prolyl isomerase activity: *fkpA* and *tig* (trigger factor). FkpA is a periplasmic protein that is a member of the FK506-binding protein family [Horne and Young, *Arch Microbiol.* 163:357-65 (1995); Missiakas, *et al.*, *Mol Microbiol.* 21:871-84 (1996)]. FkpA has been shown to contribute to intracellular survival of  
10 *Salmonella typhimurium* [Horne, *et al.*, *Infect Immun.* 65:806-10 (1997)] and a *Legionella pneumophila* homolog, *mip* [Engleberg, *et al.*, *Infect Immun.* 57:1263-1270 (1989)], is responsible for virulence and infection of macrophages [Cianciotto, *et al.*, *J. Infect. Dis.* 162:121-6 (1990); Cianciotto, *et al.*, *Infect. Immun.* 57:1255-1262 (1989)]. Tig, or trigger factor [Crooke and Wickner, *Proc. Natl. Acad. Sci. USA.* 84:5216-20 (1987), Guthrie, and Wickner, *J Bacteriol.* 172:5555-62 (1990), reviewed  
15 in Hesterkamp, and Bukau., *FEBS Lett.* 389:32-4 (1996)], is a peptidyl prolyl isomerase containing a typical FKBP region [Callebaut and Mornon, *FEBS Lett.* 374:211-215 (1995)], but is unaffected by FK506 [Stoller, *et al.*, *EMBO J.* 14:4939-48 (1995)]. Tig has been shown to associate with the ribosomes and nascent polypeptide  
20 chains [Hesterkamp, *et al.*, *Proc Natl Acad Sci USA* 93:4437-41 (1996), Stoller, *et al.*, *EMBO J.* 14:4939-48 (1995)]. Possible roles include an unknown influence on cell division [Guthrie, and Wickner, *J Bacteriol.* 172:5555-62 (1990)] in *E. coli*, a role in the secretion and activation of the *Streptococcus pyogenes* cysteine proteinase [Lyon, *et al.*, *EMBO J.* 17:6263-75 (1998)] and survival under starvation conditions in  
25 *Bacillus subtilis* [Gothel, *et al.*, *Biochemistry* 37:13392-9 (1998)].

Bacterial pathogens employ many mechanisms to coordinately regulate gene expression in order to survive a wide variety of environmental conditions within the host. Differences in mRNA stability can modulate gene expression in prokaryotes [Belasco and Higgins, *Gene* 72:15-23 (1988)]. For example, *rnr* (*vacB*) is required  
30 for expression of plasmid borne virulence genes in *Shigella flexneri* [Tobe, *et al.*, *J*

*Bacteriol.* 174:6359-67 (1992)] and encodes the RnaseR ribonuclease [Cheng, *et al.*, *J. Biol. Chem.* 273:14077-14080 (1998)]. PNP is a polynucleotide phosphorylase that is involved in the degradation of mRNA. Null *pnp* / *rnr* mutants are lethal, suggesting a probable overlap of function. It therefore is possible that both *rnr* and *pnp* are  
5 involved in the regulation of virulence gene expression. A *pnp* mutant of *P. multocida* is avirulent in a mouse septicemic model (Example 2)]. Other *pnp*-associated phenotypes include competence deficiency and cold sensitivity in *Bacillus subtilis* [Wang and Bechhofer, *J Bacteriol.* 178:2375-82 (1996)].

HupA is a bacterial histone-like protein, which in combination with  
10 HupB constitute the HU protein in *E. coli*. Reports have suggested that *hupA* and *hupB* single mutants do not demonstrate any observable phenotype [Huisman, *et al.*, *J Bacteriol.* 171:3704-12 (1989), Wada, *et al.*, *J Mol Biol.* 204:581-91 (1988)], however, *hupA-hupB* double mutants have been shown to be cold sensitive, sensitive to heat shock and blocked in many forms of site-specific DNA recombination [Wada,  
15 *et al.*, *J Mol Biol.* 204:581-91 (1988), Wada, *et al.*, *Gene.* 76:345-52 (1989)]. One limited data previously indicated that *hupA* is directly involved in virulence [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)]. The mechanism of *hupA* attenuation remains unknown.

DnaK is a well known and highly conserved heat shock protein  
20 involved in regulatory responses to various stressful environmental changes [reviewed in Lindquist and Craig, *Annu Rev Genet.* 22:631-77 (1988)]. DnaK is also one of the most significantly induced stress proteins in *Yersinia enterocolitica* after being phagocytosed by macrophages [Yamamoto, *et al.*, *Microbiol Immunol.* 38:295-300 (1994)] and a *Brucella suis dnaK* mutant failed to multiply within human  
25 macrophage-like cells [Kohler, *et al.*, *Mol Microbiol.* 20:701-12 (1996)]. In contrast, another intracellular pathogen, *Listeria monocytogenes*, did not show induction of *dnaK* after phagocytosis [Hanawa, *et al.*, *Infect Immun.* 63:4595-9 (1995)]. A *dnaK* mutant of *Vibrio cholera* affected the production of ToxR and its regulated virulence factors in vitro but similar results were not obtained from in vivo grown cells  
30 [Chakrabarti, *et al.*, *Infect Immun.* 67:1025-1033 (1999)]. The CI of *A.*

*pleuropneumonia dnaK* mutant was higher than most of the attenuated mutants although still approximately half of the positive control strain.

DksA is a dosage dependent suppressor of filamentous and temperature-sensitive growth in a *dnaK* mutant of *E. coli* [Kang and Craig, *J Bacteriol.* 172:2055-64 (1990)]. There is currently no defined molecular function for DksA, but the gene has been identified as being critical for the virulence of *Salmonella typhimurium* in chickens and newly hatched chicks [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)]. In that work, it was noted that the *dksA* mutant did not grow well with glucose or histidine but did grow well with glutamine or glutamate as the sole carbon source. This observation may indicate that the *dksA* mutant is somehow impaired in the biosynthesis of glutamate [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)].

Three genes were identified that have roles in protein synthesis: tRNA-leu, tRNA-glu and *rpmF*. Excluding protein synthesis, tRNA's also have a wide variety of functional roles in peptidoglycan synthesis [Stewart, *et al.*, *Nature* 230:36-38 (1971)], porphyrin ring synthesis [Jahn, *et al.*, *Trends Biochem Sci.* 17:215-8 (1992)], targeting of proteins for degradation [Tobias, *et al.*, *Science* 254:1374-7 (1991)], post-translational addition of amino acids to proteins [Leibowitz and Soffer, *B.B.R.C.* 36:47-53 (1969)] and mediation of bacterial-eukaryotic interactions [Gray, *et al.*, *J Bacteriol.* 174:1086-98 (1992), Hromockyj, *et al.*, *Mol Microbiol.* 6:2113-24 (1992)]. More specifically, tRNA-leu is implicated in transcription attenuation [Carter, *et al.*, *Proc. Natl. Acad. Sci. USA* 83:8127-8131 (1986)], lesion formation by *Pseudomonas syringae* [Rich and Willis, *J Bacteriol.* 179:2247-58 (1997)] and virulence of uropathogenic *E. coli* [Dobrindt, *et al.*, *FEMS Microbiol Lett.* 162:135-141 (1998), Ritter, *et al.*, *Mol Microbiol.* 17:109-21 (1995)]. It is unknown whether the tRNA that we have identified represents a minor species of tRNA-leu in *A. pleuropneumoniae*. Regardless, it is possible that tRNA-leu may have any one of a wide range of functions. RpmF is a ribosomal protein whose gene is also part of an operon containing fatty acid biosynthesis enzymes in *E. coli*. Further work will be required to indicate if this is the case in *A. pleuropneumoniae*, although the same

clustering of *fab* genes and *rpmF* occurs in *Haemophilus influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)]. The expression of the *fab* genes is not necessarily dependent on transcripts originating upstream of *rpmF* as there has been a secondary promoter identified within *rpmF* [Zhang and Cronan, Jr., *J Bacteriol.* 180:3295-303 (1998)].

The final class of attenuated mutants includes mutations within genes of unknown function or genes that have not been previously identified. Homologs of *yaeA* and HI0379 have previously been identified in *Escherichia coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)] and *Haemophilus influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)], respectively. The remaining unknowns have been designated *Actinobacillus pleuropneumoniae* virulence genes (*apv*). The *apvC* gene shows significant similarity to HI0893, however, the proposed similarity of HI0893 as a transcriptional repressor similar to the fatty acid response regulator Bm3R1 [Palmer, *J Biol Chem.* 273:18109-16 (1998)] is doubtful. The *apvD* gene is also most similar to a putative membrane protein (b0878) with unknown function from *E. coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)]. Two other unknowns, *apvA* and *apvB* had no significant matches in the public databases.

#### Example 11

##### Safety and Efficacy of *A. pleuropneumoniae* Mutants

Nine groups (n=8) of SPF pigs (4-5 weeks old, 3-10 kg) were used to determine the safety and efficacy of seven *A. pleuropneumoniae* mutants as live attenuated vaccine strains. Seven groups were infected intranasally with  $10^{10}$  CFU of each mutant on day 1. One group was vaccinated on days 1 and 15 with the commercially available vaccine Pleuromune (Bayer), and one naive group was not vaccinated. On day 29, all groups were challenged intranasally with  $1-5 \times 10^5$  CFU per pig of wild type APP225. All surviving animals were euthanized and necropsied on day 42 of the study. Results are shown in Table 4.

**Table 4**  
**Efficacy of *A. pleuropneumoniae* Mutants**

	<u>Vaccine</u>	% Mortality following intranasal challenge	
		<u>Vaccination</u>	<u>Challenge</u>
5	Pleuromune	0	37.5
	exbB	0	0
	tig	12.5	0
	fkpA	12.5	0
	HI0385	50.0	0
10	pnp	0	0
	yaeE	0	0
	atpG	0	0
	None	N/A	50.0

15                   The *exbB*, *atpG*, *pnp*, and *yaeA* mutants caused no mortality when administered at a dosage of  $10^{10}$  CFU intranasally. The *fkpA* and *tig* mutant groups had one death each and the HI0379 group (highest CI of the 7 mutants tested shown in Example 9) had four deaths. Wildtype LD<sub>50</sub> using this model was generally  $1 \times 10^7$  CFU, indicating that each of these mutants is at least 100 fold attenuated and that

20                   there is a reasonable correlation between CI and attenuation.

**Example 12**  
**Identification of *P.(Mannheimia) haemolytica* Species Homologs**

25                   Based on the sequences of virulence genes identified in *P. multocida* and *A. pleuropneumoniae*, attempt were made to identify related genes, i.e., species homologs, in *P. (Mannheimia) haemolytica*. PCR was utilized with the degenerate primers shown below to attempt amplification of the *P. (Mannheimia) haemolytica* genes as indicated. Primer sequences, synthesized by Sigma-Genosys (The Woodlands, TX), include standard single letter designations, wherein B indicates

either (C,G or T), D indicates either (G,A or T), H indicates either (A,C or T), K indicates either (G or T), M indicates either (A or C), N indicates either (A,G,C or T), R indicates either (A or G), S indicates either (G or C), V indicates either (G, A, or C), W indicates either (A or T), and Y indicates either (C or T).

5

atpG	TEF146	ATG GCN GGN GCN AAR GAR AT	SEQ ID NO: 176
	TEF148	GCN GCY TTC ATN GCN ACC AT	SEQ ID NO: 177

10

guaB	TEF240	GGN TTY ATY CAY AAA AAY ATG	SEQ ID NO: 178
	TEF243	TCT TTN GTR ATN GTN ACA TCR TG	SEQ ID NO: 179

pnp	TEF141	GCS GGY AAA CCR CGT TGG GAT TGG	SEQ ID NO: 180
	TEF142	CRC CTA ARA TRT CTG AAA GCA CCA C	SEQ ID NO: 181

15

purF	TEF244	ATG TGY GGN ATY GTN GGN AT	SEQ ID NO: 182
	TEF247	CAT ATC AAT ACC ATA CAC ATT	SEQ ID NO: 183

yjgF	TEF162	GGN CCN TAY GTN CAR G	SEQ ID NO: 184
	TEF163	NGC NAC YTC NAC RCA	SEQ ID NO: 185

20

For amplification of initial degenerate PCR products, a 50 µl reaction was set up using 3.3X XL buffer II (PE Applied Biosystems), 200 µM dNTPs, 25 pmol each of the appropriate primers, 0.8 mM MgCl<sub>2</sub>, 0.5 U *rTth* DNA polymerase, XL (PE Applied Biosystems) and approximately 1 µg of TF1 DNA.

25

Cycle conditions were 94°C for 1.5 min; followed by 35 cycles of 94°C for 15 s, 40-60°C for 60 s, 72°C for 1.5 min; and a final hold at 72°C for 5 min. Each PCR product was band purified from an agarose gel using the QIAGEN Gel Extraction Kit (QIAGEN, Valencia CA).

30

Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 DNA Sequencer. Double stranded sequence for the open reading frame (ORF) for each clone was obtained. Sequencher 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs were used to confirm the identity of the ORF by searching for homologous sequences in currently available databases.

35

The Vectorette Kit (Genosys Biotechnologies, The Woodlands, TX) was used to obtain additional flanking sequence for each of the genes. Vectorette libraries were prepared according to the manufacturer's suggested protocol. Perkin Elmer Applied Biosystems GeneAmp XL PCR Kit components were used to create the

5 Vectorette PCR products with the following reaction conditions. A 50  $\mu$ l reaction was set up using 3.3X XL buffer II (PE Applied Biosystems), 200  $\mu$ M dNTPs, 25 pmol each of the appropriate primers(shown below), 0.8 mM  $MgCl_2$ , 0.5 U *rTth* DNA polymerase, XL (PE Applied Biosystems) and 1  $\mu$ l of the appropriate vectorette library. Cycle

10 conditions were 94°C for 1.5 min; followed by 35 cycles of 94°C for 20 s, 60°C for 45s, 72°C for 4 min; and a final hold of 72°C for 7 min. The second primer for each library was the manufacturer's vectorette primer.



Table 5

Gene	Vectorette library	Primer(s)
atpG	BglII, HindIII	TEF217 GAAGCCGCCATACGCTCTTGGG SEQ ID NO: 186
	ClaI	TEF218 GTTGCTTCCTTTGCCTGCACTGG SEQ ID NO: 187
guaB	EcoRI	TEF265 GGCTCAGAAACAATACCACTTTCA SEQ ID NO: 188
	HindIII, TaqI	TEF268 GCACCAAAGCAGAATTTGTCC SEQ ID NO: 189
pnp	ClaI, HincII	TEF219 GGTGATGATGTGCGATGATAGTCCC SEQ ID NO: 190
	TaqI,	TEF220 GGCGTATTAGCCGTGATGCCAACC SEQ ID NO: 191
	BamHI	TEF286 GACCACTTAGGCGATATGGACTT SEQ ID NO: 192
purF	TaqI	TEF271 ACCATCATAAATCGCCTGATTC SEQ ID NO: 193 TEF292 ACCTGCGGCATCTTGTCCCTC SEQ ID NO: 194
	HincII	TEF274 ACGGGTTTATTTTGCCTCTG SEQ ID NO: 195
yjgF	ClaI	TEF221 CGCCGGTTTCAGGATTCACGGG SEQ ID NO: 196
	EcorV	TEF281 CTGAACAACGTGAAAGCCAT SEQ ID NO: 197

Vectorette PCR products were band purified and sequenced as described above.

Polynucleotide sequences for the atpG, guaB, pnp, purF, and yjgF genes are set out in SEQ ID NOs: 166, 168, 170, 172 and 174, respectively. Polypeptides encoded by these genes are set out in SEQ ID NOs: 167, 169, 171, 173, and 175, respectively.

;

Numerous modifications and variations in the invention as set forth in the above illustrative examples are expected to occur to those skilled in the art. Consequently only such limitations as appear in the appended claims should be placed on the invention.

## WHAT IS CLAIMED IS:

1. A gram-negative bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120, 122, 124, 126, 128, and 130, or species homologs thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

2. The gram-negative bacteria of claim 1 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

3. The gram-negative bacteria of claim 1 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

4. The gram-negative bacteria of claim 1 wherein said mutation results in deletion of all or part of said gene.

5. An attenuated *Pasteurellaceae* bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

6. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

7. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

8. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in deletion of all or part of said gene.

9. The *Pasteurellaceae* bacteria of claim 5 selected from the group consisting of *Pasteurella (Mannheimia) haemolytica*, *Pasteurella multocida*, *Actinobacillus pleuropneumoniae* and *Haemophilus somnus*.

10. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

11. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

12. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in deletion of all or part of said gene.

13. The attenuated *Pasteurellaceae* bacteria of claim 9 that is a *P. multocida* bacteria.

14. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

15. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

16. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in deletion of all or part of said gene.

17. The attenuated *Pasteurellaceae* bacteria of claim 9 that is a *A. pleuropneumoniae* bacteria.

18. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

19. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

20. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in deletion of all or part of said gene.

21. An immunogenic composition comprising the bacteria according to any one of claims 1 through 20.

22. A vaccine composition comprising the immunogenic composition according to claim 21 and a pharmaceutically acceptable carrier.

23. The vaccine composition according to claim 22 further comprising an adjuvant.

24. A method for producing a gram-negative bacteria mutant comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

25. A method for producing an attenuated *Pasteurellaceae* bacteria comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29,

31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

26. A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174.

27. A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120, 122, 124, 126, 128, and 130.

28. A purified and isolated polynucleotide encoding a *Pasteurellaceae* virulence gene product, or species homolog thereof, selected from the group consisting of:

- a) the polynucleotide according to claim 27,
- b) polynucleotides encoding a polypeptide encoded by the polynucleotide of (a), and
- c) polynucleotides that hybridize to the complement of the polynucleotides of (a) or (b) under moderate stringency conditions.

29. A purified and isolated *Pasteurellaceae* polynucleotide encoding a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109,

111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175.

30. The polynucleotide of claim 29 which is a DNA.

31. A vector comprising the DNA of claim 30.

32. The vector of claim 31 that is an expression vector, wherein the DNA is operatively linked to an expression control DNA sequence.

33. A host cell stably transformed or transfected with the DNA of claim 30 in a manner allowing the expression of the encoded polypeptide in said host cell.

34. A method for producing a recombinant polypeptide comprising culturing the host cell of claim 33 in a nutrient medium and isolating the encoded polypeptide from said host cell or said nutrient medium.

35. A purified polypeptide produced by the method of claim 34.

36. A purified polypeptide comprising a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175.

37. An antibody that is specifically reactive with the polypeptide of claim 36.

38. The antibody of claim 33 that is a monoclonal antibody.

39. A method of using the monoclonal antibody of claim 39 for identifying a bacteria of claim 1, 5, 9, or 13 comprising the step of contacting an extract of bacteria with said monoclonal antibody and detecting the absence of binding of said monoclonal antibody.

40. A method of identifying an anti-bacterial agent comprising the steps of assaying potential agents for the ability to interfere with expression or activity of gene products represented by the amino acid sequences set forth in any one of SEQ ID NOS: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175 and identifying an agent that interferes with expression or activity of said gene products.

41. A method of identifying an anti-bacterial agent comprising the steps of:

- a) measuring expression or activity of a gene product as set out in SEQ ID NOS: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175;
- b) contacting the gene product in (a) with a test compound
- c) measuring expression or activity of the gene product in the presence of the test compound; and
- d) identifying the test compound as an antibacterial agent when expression or activity of the gene product is decreased in the presence of the test compound as compared to expression or activity in the presence of the test compound.



## SEQUENCE LISTING

<110> Lowery E., David, et al.

<120> Anti-Bacterial Vaccine Compositions

<130> 28341/00435

<140> 09/809,665

<141> 2001-03-15

<150> 60/153,453

<151> 1999-09-10

<150> 60/128,689

<151> 1999-04-09

<150> 09/545,199

<151> 2000-04-06

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15

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60 65 70

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Asp Gly Ile Val Lys Glu Asn Phe His Gly Pro Arg His Ala Val Gly
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155 160 165

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170 175 180

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                     165                    170                    175  
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 Ala Phe Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile  
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 Gly Ile Phe Met His Leu Ala Trp Ala Ile Phe His Ile Leu Val Ile  
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 atg cgt aaa acg caa gaa cgc atg tct tct tca cgc cct tat tca gaa 504  
 Met Arg Lys Thr Gln Glu Arg Met Ser Ser Ser Arg Pro Tyr Ser Glu  
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 Thr Ile Arg Asn Val Ile Ser His Val Ser Lys Ala Thr Ile Gly Tyr  
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 Lys His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile  
 65 70 75  
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 80 85 90 95  
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 Phe Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val  
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 ccc tct gtt gag cag tta att ggt tca gtc aat tct atg att gat gct 840  
 Pro Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala  
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195 200 205

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Tyr Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val
210 215 220

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225 230 235

tct gag caa gcc gct cga atg gtc gcc atg aaa gca gca aca gat aac 1128
Ser Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn
240 245 250 255

gca ggt aac tta att aat gag tta cag tta gtc tat aac aaa gct cgt 1176
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260 265 270

caa gca agt att aca aat gaa tta aat gaa att gtt gcc ggt gca gca 1224
Gln Ala Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala
275 280 285

gca att taacaaatag aggatcggta atggcaactg gaaaaattgt acaaatcatc 1280
Ala Ile

ggtgcgggtta ttgacgttga attcccacaa gatgcagtac caaaagtata tgatgcctta 1340

aatggttga aa caggttttagt acttgaagtt caacaacaat taggtggtgg tgtagttcgc 1400

tgtatcgcaa tgggatcatc tgatggatta aaacgcggtt taagcgtaac aaatacgaat 1460

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His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile Val	65	70	75
Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Val Asn Leu Phe	85	90	95
Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val Ser	100	105	110
Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln Ser	115	120	125
Leu Gly Ile Lys Ile Leu Thr Gln Asp Ser Gly Ile Gly Asp Thr Pro	130	135	140
Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala Tyr	145	150	155
Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe Ile	165	170	175
Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu Pro	180	185	190
Glu Leu Asp Asn Asp Glu Leu Gly Glu Arg Lys Gln Val Trp Asp Tyr	195	200	205
Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val Arg	210	215	220
Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala Ser	225	230	235
Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala	245	250	255
Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln	260	265	270
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Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr	
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145 150 155 160	
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Leu Ala Lys Ala Ile Thr Glu Leu Leu Ser Val Pro Asn His Pro Ile	
165 170 175	
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Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg	
195 200 205	
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Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys	
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Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu
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Gly Thr Pro Thr Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala
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Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly
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Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr
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Val His Ile Ser Leu Ser Gly Gly Ser Thr Pro Lys Leu Leu Phe Lys
          30             35             40             45

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Thr Leu Ala Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu
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Ser Asn Tyr Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile
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cct gca gaa aat att cac cgc att cgt ggt gaa gcc ccc gtt gag agt 4358
Pro Ala Glu Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser
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Val Phe Asp Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala
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tca tta ttc ccg cat caa acc gat ttt gac gat cct cat ttc gcc gtg 4502
Ser Leu Phe Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val
     145              150             155

atc gcg aaa cac cct gaa aca ggg caa att cgt att tca aaa aca gcg 4550
Ile Ala Lys His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala
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aaa ttg att gaa caa gca aag cgg gtg acc tat ttg gtg aca ggt agc 4598
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Ser Lys Ala Glu Ile Leu Lys Glu Ile Gln Thr Thr Pro Ala Glu Gln
     190              195             200             205

ctg cct tat cct gct gcg aaa atc aaa gcg aag cat ggg gtg acg gaa 4694
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Trp Tyr Leu Asp Lys Asp Ala Ala Lys Leu Leu
     225              230

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&lt;211&gt; 232

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 8

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 Ser Leu Ser Gly Gly Ser Thr Pro Lys Leu Leu Phe Lys Thr Leu Ala  
 35 40 45  
 Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu His Phe Trp  
 50 55 60  
 Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu Ser Asn Tyr  
 65 70 75 80  
 Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile Pro Ala Glu  
 85 90 95  
 Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser Glu Leu His  
 100 105 110  
 Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln Val Phe Asp  
 115 120 125  
 Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala Ser Leu Phe  
 130 135 140  
 Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val Ile Ala Lys

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			180					185					190		
Glu	Ile	Leu	Lys	Glu	Ile	Gln	Thr	Thr	Pro	Ala	Glu	Gln	Leu	Pro	Tyr
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                  1                      5                      10

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Pro Phe Phe Asp Phe Val Gly Cys Phe Leu Leu Glu Asn Phe Gln Leu
      15                      20                      25

cct ttg cct att cat caa ctc gat gat gaa acg ctg gat aat ttc tat 1766
Pro Leu Pro Ile His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr
      30                      35                      40

ccc gac aat aat tta ttg ttg ctc aat tcg cta cgc aaa aat ttt act 1814
Pro Asp Asn Asn Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr
      45                      50                      55                      60

tgt cta aca caa caa ttt ttt tat att tgg ggc gag caa agc agt ggt 1862
Cys Leu Thr Gln Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly
      65                      70                      75

aaa agt cac ctc tta aaa ggc att act cat cat ttt ttc ctt tta cag 1910
Lys Ser His Leu Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln
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cgc ccc gct atc tat gtg ccc tta gaa aaa tcc caa tat ttc tca ccg 1958
Arg Pro Ala Ile Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro
      95                      100                      105

gcg gta ctc gaa aac tta gaa caa caa caa ttg gtt tgt tta gat aat 2006
Ala Val Leu Glu Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn
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tta cag gca att ata ggc aat act gaa tgg gaa tta gcg att ttt gat 2054
Leu Gln Ala Ile Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp
      125                      130                      135                      140

tta ttt aat cgc ata aaa tct gtt gaa aat aca ctg ctt gtg atc agt 2102
Leu Phe Asn Arg Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser
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gca aat caa tcc cca act gca tta cct gta agt tta cct gac tta gct 2150

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Ser Arg Leu Arg Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp  
175 180 185

caa caa aaa atc cat gta ttg caa aaa aat gca cat caa cgt ggt atc 2246  
Gln Gln Lys Ile His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile  
190 195 200

gaa ctc ccc gat gaa gta gct aat ttt ctt ttg aaa cgc tta gag cgc 2294  
Glu Leu Pro Asp Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg  
205 210 215 220

gat atg aaa acg tta ttt gaa gca cta agt aaa tta gat aaa gca tca 2342  
Asp Met Lys Thr Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser  
225 230 235

tta caa gcc caa cgt aaa tta acg att ccc ttt gta aaa gaa att tta 2390  
Leu Gln Ala Gln Arg Lys Leu Thr Ile Pro Phe Val Lys Glu Ile Leu  
240 245 250

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Lys Leu

&lt;210&gt; 10

&lt;211&gt; 254

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 10

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Phe Val Gly Cys Phe Leu Leu Glu Asn Phe Gln Leu Pro Leu Pro Ile  
20 25 30

His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr Pro Asp Asn Asn  
35 40 45

Leu Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr Cys Leu Thr Gln  
50 55 60

Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly Lys Ser His Leu  
65 70 75 80

Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln Arg Pro Ala Ile  
85 90 95

Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro Ala Val Leu Glu  
100 105 110

Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn Leu Gln Ala Ile  
115 120 125

Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp Leu Phe Asn Arg  
130 135 140

Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser Ala Asn Gln Ser  
145 150 155 160



Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala Ser Arg Leu Arg  
                           165                          170                          175

Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp Gln Gln Lys Ile  
                           180                          185                          190

His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile Glu Leu Pro Asp  
                           195                          200                          205

Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg Asp Met Lys Thr  
                           210                          215                          220

Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser Leu Gln Ala Gln  
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Arg Lys Leu Thr Ile Pro Phe Val Lys Glu Ile Leu Lys Leu  
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                           1                          5                          10

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agt gca tgg ttt cta ttg ttt agc tca gct tta cta tta gag gct atc 939
Ser Ala Trp Phe Leu Leu Phe Ser Ser Ala Leu Leu Leu Glu Ala Ile
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gct ctt tat ttt caa cat ggc atg ggg ctc gcc cct tgt gtc atg tgt 987
Ala Leu Tyr Phe Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys
      30                35                40

att tac gag agg gta gct att ctt ggc att gct ttc tcc ggt tta ttg 1035
Ile Tyr Glu Arg Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu
      45                50                55                60

ggg tta ctc tac ccg agt tcg atg ctt ttg cgc ctt gtg gcg tta tta 1083
Gly Leu Leu Tyr Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu
      65                70                75

att ggt tta agc agt gca atc aaa ggc tta atg att agc atc acc cat 1131
Ile Gly Leu Ser Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His
      80                85                90

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Leu Asp Leu Gln Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val
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gca gaa ttt ccc gag act tta ccc tta gat cag tgg ttt cct gca ctc 1227
Ala Glu Phe Pro Glu Thr Leu Pro Leu Asp Gln Trp Phe Pro Ala Leu
      110                115                120

ttc ctc cct tca ggc tca tgc agt gaa gta aca tgg caa ttt ctc ggc 1275
Phe Leu Pro Ser Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly
      125                130                135                140

ttt tct atg gtg caa tgg atc gtc gtc att ttt gca ctc tat acc tta 1323
Phe Ser Met Val Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu
      145                150                155

tta ctt gct ctc att ttc atc agc caa gtc aaa cgt cta aaa ccc aag 1371
Leu Leu Ala Leu Ile Phe Ile Ser Gln Val Lys Arg Leu Lys Pro Lys
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ggcgcgcatac taacaaatgc cctaatacca tattatacgc cgctaaggca aaccaaatac 1959

gctcatcttc tttaatcgta tcaggcattt gcgtaataag ccaatgtaaa tattctgaac 2019

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<213> Pasteurella multocida

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20 25 30

Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys Ile Tyr Glu Arg  
35 40 45

Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu Gly Leu Leu Tyr  
50 55 60

Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu Ile Gly Leu Ser  
65 70 75 80

Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His Leu Asp Leu Gln  
85 90 95

Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val Ala Glu Phe Pro  
100 105 110

Glu Thr Leu Pro Leu Asp Gln Trp Phe Pro Ala Leu Phe Leu Pro Ser  
115 120 125

Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly Phe Ser Met Val  
130 135 140

Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu Leu Leu Ala Leu  
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Phe His

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<212> DNA

<213> Pasteurella multocida

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Gly Leu Leu Ala Phe Met Ser Phe Ile Met Val Trp Leu Val Ile Glu						
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cgc ttt ctt ttc tta agt cgc gtc aac gtg gca tct tat gaa agc ata						2902
Arg Phe Leu Phe Leu Ser Arg Val Asn Val Ala Ser Tyr Glu Ser Ile						
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cat gaa tta gac att gac tta caa cgc cac ctc aca gct atc tct aca						2950
His Glu Leu Asp Ile Asp Leu Gln Arg His Leu Thr Ala Ile Ser Thr						
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Ile Gly Ser Asn Ala Pro Tyr Val Gly Leu Leu Gly Thr Val Ile Gly						
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att ctc tta act ttc tat gaa tta ggt cac tcc ggt ggc gat att gat						3046
Ile Leu Leu Thr Phe Tyr Glu Leu Gly His Ser Gly Gly Asp Ile Asp						
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gcg gcg gcc att atg gtg cac tta tca tta gcc tta aaa gcc aca gca						3094
Ala Ala Ala Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr Ala						
	100				105	110
gta ggt att tta gtc gcc att cct gca atg gtg tgt tac aac ggt tta						3142
Val Gly Ile Leu Val Ala Ile Pro Ala Met Val Cys Tyr Asn Gly Leu						
	115				120	125
gga cgt aaa gtc gaa gtt aat cgt ttg aaa tgg ttt gcc tta aat gag						3190
Gly Arg Lys Val Glu Val Asn Arg Leu Lys Trp Phe Ala Leu Asn Glu						
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Lys Lys Ala Lys Gln Gln Ala  
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<213> Pasteurella multocida

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Glu Arg Phe Leu Phe Leu Ser Arg Val Asn Val Ala Ser Tyr Glu Ser  
35 40 45

Ile His Glu Leu Asp Ile Asp Leu Gln Arg His Leu Thr Ala Ile Ser  
50 55 60

Thr Ile Gly Ser Asn Ala Pro Tyr Val Gly Leu Leu Gly Thr Val Ile

65		70		75		80
Gly Ile Leu Leu Thr Phe Tyr Glu Leu Gly His Ser Gly Gly Asp Ile						
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Asp Ala Ala Ala Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr						
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Ala Val Gly Ile Leu Val Ala Ile Pro Ala Met Val Cys Tyr Asn Gly						
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 5 10 15  
 gaa aac ggt tta ttc cat aca ctc ggt aat atg atg tta gaa gca gag 632  
 Glu Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu  
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 cgt tct gtt tat aat att ggc gat att tat gcg agt aaa aaa tta aca 680  
 Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr  
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Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val	
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Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val	
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Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu	
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Gln Glu Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile	
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Arg Ser Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser	
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Glu Ser Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly	
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aca ttt aat gcg gaa gct gat caa gtg gtg aac caa atg aaa gcg ttt	1016
Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe	
150 155 160	
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Asn Gln Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr	
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210 215 220 225	
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Phe Ser Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr	
230 235 240	
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Tyr Asp Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr	
260 265 270	
gat ttc att tat tac cca tca gaa aaa gca aaa atc cta gcg gga aaa	1400
Asp Phe Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys	
275 280 285	
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Leu Glu Gly Lys Leu Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg	
290 295 300 305	



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Gly Lys Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu	
310 315 320	
cca tca gta gag ctt aaa gcg gag ttt agt gat aaa gaa cgt ttg gaa	1544
Pro Ser Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu	
325 330 335	
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Glu Asp Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro	
340 345 350	
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Glu Ser His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp	
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Glu Ser Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys	
405 410 415	
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Glu Met Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn	
420 425 430	
aaa cca cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa	1880
Lys Pro Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu	
435 440 445	
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Glu Glu Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr	
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Gln Glu Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys	
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cat caa gtg att act cgc tcg att gag aaa aaa gta gat aac cac ctt His Gln Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu 710 715 720	2696
aac caa aaa tac aat ctc agc gat gtg gaa tta gtt aaa cag ctg atg Asn Gln Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met 725 730 735	2744
gac aat tcc aca aca caa gcg cag gag ttg gat ttg aaa cta ggt gcg Asp Asn Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala 740 745 750	2792
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Arg	Leu	Val	Gly	Arg	Lys	Gly	Ile	Glu	Asn	Val	Ser	Arg	Ser	Phe	Ala	
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Asn	Asp	Glu	Leu		Val	Thr	Ala	Gln	Arg	Ser	Glu	Ile	Lys	Thr	Glu	
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Gly	His	Leu	His	Leu	Glu	Thr	Asp	Lys	Asp	Ser	Thr	Ile	Asp	Val	Gln	
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Ala	Ser	Asp	Ile	Lys	Ala	Lys	Thr	Ser	Phe	Val	Lys	Thr	Gly	Asp	Val	
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Ser	Pro	Ser	Ala	Leu		Gln	Val	Ala	Glu	Leu	Asp	Val	Ala	Gly	Leu	
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Val	Pro	Leu	Leu	Gly	Val	Ser	Ser	Pro	Ser	Ser	Tyr	Ser	Glu	His	Thr	
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Ser	Glu	Ala	Thr	Ser	Glu	Gly	Ser	Ile	Phe	Glu	Val	Gly	His	Leu	His	
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Leu	Ala	Val	Asp	Arg	Asp	Val	Asn	Gln	Ala	Gly	Ser	Lys	Ile	Lys	Ala	
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Ala	Ser	Ala	His	Ala	Ser	Gly	Gly	Gly	Thr	Ser	Val	Arg	Tyr	Asp	Tyr	
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Thr	Gly	Val	Gly	Ala	Glu	Ala	Gly	Met	Ser	Phe	Thr	His	Thr	Lys	Asp	
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Asp Leu Ala Gly Ser Ser Ala Lys Leu Ser Val Glu Arg Thr His Glu	
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Thr Lys Arg Thr Thr Glu Thr Gly Asp Ile Val Thr Lys Ile Gly Gly	
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Tyr Thr Ser Glu Arg Glu Thr Ala Gln Asn Asn Ser Phe Leu Lys Ala	
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Pro Thr Gly Asn Val Gly Phe Gly Tyr Thr Asn Glu Thr Glu Ser Lys	
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Ser Arg Val Thr Asp Glu Ala Asp Ser Val Ser Val Lys Asn Pro Ile	
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Thr Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn  
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Val Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg  
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Val Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn  
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Leu Gln Glu Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala  
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Ile Arg Ser Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser  
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Ser Glu Ser Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys  
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Gly Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala  
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Phe Asn Gln Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile  
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Thr Met Tyr Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser  
           180                  185                  190

Gly Asn Ala Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala  
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Leu Phe Gly Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu  
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Asn Phe Ser Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met  
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Tyr Gln Lys Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys  
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Ser Tyr Asp Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro  
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Thr Asp Phe Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly  
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 Lys Leu Glu Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu  
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 Arg Gly Lys Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser  
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 770 775 780  
 Val Tyr Phe Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly  
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Lys Val Pro Leu Leu Gly Val Ser Ser Pro Ser Ser Tyr Ser Glu His  
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 Thr Ser Glu Ala Thr Ser Glu Gly Ser Ile Phe Glu Val Gly His Leu  
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Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser Ala Val Phe Asn Asn Asn	
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Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu Ile Gly Tyr Ile Pro Gln	
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Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala Asp Val Ile Leu Asn Gln	
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Val Thr Gly Pro Gln Glu Ser Lys Ile Val Gly Ala Leu Glu Val Leu	
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Gly Lys Lys Ala Asp Ile Val Ile Ala Asn Gln Asn Gly Ile Thr Leu	
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Asn Gly Val Arg Thr Ile Asn Ser Asp Arg Phe Val Ala Thr Thr Ser	
235 240 245	
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Glu Leu Ile Asp Pro Asn Gln Met Leu Lys Val Thr Lys Gly Asn	
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Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys Gln Ser Ile Thr Ser Gly	
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Glu Tyr Asp Leu Ser Lys His Glu Leu Lys Lys Thr Ser Gly Glu Asn	
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Val Ser Asn Asp Val Ile Ala Ile Thr Gly Ser Ser Thr Gly Ala Met	
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Lys His Asp Gly Ile Ile Leu Ser Glu Asn Asp Ile Gln Ile Glu Met	
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Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr Ile Gln Gln Thr Val Val	
375 380 385 390	



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 Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile  
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 Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val  
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 Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg  
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 Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys  
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His Ala Tyr Gln Asn Gln Pro Leu Ser Thr Lys Val Val Phe Gln Leu	
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Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser	
35 40 45	
gca att ggt tta aaa aat tca aaa atc agc aat ggc gat ctt gaa ttt	192
Ala Ile Gly Leu Lys Asn Ser Lys Ile Ser Asn Gly Asp Leu Glu Phe	
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Ile Val Leu Trp Gly Arg Thr Arg Asp Leu Phe Val Asn Gly Glu Lys	
65 70 75 80	
cca acc cgt ttt aga gat aaa aca atg tta tca gtc cta ccc aat tta	288
Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu	
85 90 95	
atc gga aat cgc tta agt att cac gac att gac cag ttg atc gaa atc	336
Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile	
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Leu Asn Thr Thr Asn Lys Lys Ala Thr Val Asn Val Val Ala Ser Glu	
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gaa aaa ggc agc tca aat cta aat att gaa aga caa tat gat gtt ttt	432
Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe	
130 135 140	
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Pro Gln Val Ser Val Gly Phe Asn Asn Ser Gly Ala Gly Asn Asn Ala	
145 150 155 160	
aat ggg cgt aat caa gct aca ttg aat att gct tgg agt gat cta tta	528
Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu	
165 170 175	
ggc acg aat gat cgt tgg agt ttc tcg agt agt tac cgt tta tat aaa	576
Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys	
180 185 190	
aat cat cat gct aac cag caa cgc aat tat act ttg tct tac agt cag	624
Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln	
195 200 205	
cct ata ggc ttt tct aca gta gaa att aaa gca tcg gaa tct acg tat	672
Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr	
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gaa aaa gaa ctt cgc ggt ata aat act cat tct tct cat ggg aaa acc	720
Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr	
225 230 235 240	
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Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu	
245 250 255	
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Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser	
260 265 270	

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Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser	
275 280 285	
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Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser	
290 295 300	
gac att gct tac gcg aat ggg ttg aga tgg ttt ggg gcg aat tat tca	960
Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser	
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Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Leu Ser Gly Ser	
325 330 335	
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Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr	
340 345 350	
caa tta cgt att ggt gcc caa tat ggt ttt gat agt ttg tat tct gaa	1104
Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu	
355 360 365	
aat caa ttt tca att ggt gat gaa tat aca gta aga gga ttt aaa ggt	1152
Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly	
370 375 380	
ggt gcg gtt tct ggt gat agt ggt gcg tat tta tca caa aca ctg acg	1200
Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr	
385 390 395 400	
gtt cct ttt tat cca caa aaa gca tat tta tct cag gta tcc cct ttt	1248
Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe	
405 410 415	
att gga ttt gat atg ggt aaa gta cat att aaa tca aag cat aaa aca	1296
Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr	
420 425 430	
acc act tta gtc ggt ttt gcc cta ggc ttg aaa acg caa ata aag tta	1344
Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu	
435 440 445	
ttt tca tta tca tta acc tat gca caa cca atg aat ggt gtg agt ggt	1392
Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly	
450 455 460	
gtt acg caa cat cgt caa aaa ccg att tat tat ttc tca gga tca ctt	1440
Val Thr Gln His Arg Gln Lys Pro Ile Tyr Phe Ser Gly Ser Leu	
465 470 475 480	
tct ttt taatctcttt taagttaaag gattaactta atatgaacaa aaatcgttac	1496
Ser Phe	
aaactcattt ttagtcaagt caaaggttgt ctcgttcctg tggcagaatg tattaactca	1556
gctattagca atgggttcac tgattcaaca tccacatcag aacaagttga agaggaaact	1616
ttccttctag aacaatatc actttcctcc gtgtctttat tagtaaaaag cacgttcaat	1676
cctgtttcgt atgcaatgca attgacttgg aaacagcttt ctattttatt ttttaactgtg	1736

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atttctgttc ctgttttggc tgagggaaaa ggggatgaaa gaaatcaatt aacagtgatt 1796
gataatagcg atcatattaa attagatgca tctaattctg ctggtaatga taaaacaaaa 1856
atctatcaag cagaaaaata agttctgggtt attgatattg ctaaaccaaa tgggaaaggg 1916
atttcagata accgttttga aaaatttaat attccaaata gcgcgggtgtt taataataat 1976
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&lt;210&gt; 20

&lt;211&gt; 482

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 20

Val Asp Leu Ala Gly Glu Lys Val Ser Leu Asn Phe Gly Asp Ile Ile  
1 5 10 15

His Ala Tyr Gln Asn Gln Pro Leu Ser Thr Lys Val Val Phe Gln Leu  
 20 25 30  
 Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser  
 35 40 45  
 Ala Ile Gly Leu Lys Asn Ser Lys Ile Ser Asn Gly Asp Leu Glu Phe  
 50 55 60  
 Ile Val Leu Trp Gly Arg Thr Arg Asp Leu Phe Val Asn Gly Glu Lys  
 65 70 75 80  
 Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu  
 85 90 95  
 Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile  
 100 105 110  
 Leu Asn Thr Thr Asn Lys Lys Ala Thr Val Asn Val Val Ala Ser Glu  
 115 120 125  
 Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe  
 130 135 140  
 Pro Gln Val Ser Val Gly Phe Asn Asn Ser Gly Ala Gly Asn Asn Ala  
 145 150 155 160  
 Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu  
 165 170 175  
 Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys  
 180 185 190  
 Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln  
 195 200 205  
 Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr  
 210 215 220  
 Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr  
 225 230 235 240  
 Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu  
 245 250 255  
 Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser  
 260 265 270  
 Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser  
 275 280 285  
 Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser  
 290 295 300  
 Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser  
 305 310 315 320  
 Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Leu Ser Gly Ser  
 325 330 335  
 Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr  
 340 345 350

Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu  
           355                                  360                                  365  
 Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly  
           370                                  375                                  380  
 Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr  
           385                                  390                                  395                                  400  
 Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe  
                                   405                                  410                                  415  
 Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr  
                                   420                                  425                                  430  
 Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu  
           435                                  440                                  445  
 Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly  
           450                                  455                                  460  
 Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu  
           465                                  470                                  475                                  480  
 Ser Phe

<210> 21  
 <211> 1170  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <221> CDS  
 <222> (639)..(1022)

<220>  
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 aagcgttggg atcgcgcgaa ttgcgttgac cactggtgag atcgggggtca cctgtaaaac 120  
 gtacgataag atcgccatgc atttcattgt tttttatatt tccattgggt aatagactgg 180  
 tttcaaattg aaattggtca cttagtacga gtttgccggt taaggcgggt agcacttttt 240  
 gtgtactggc gggtaacata aaggtactgg cttggtgcgc tacaattttt tcattacgat 300  
 ttaagttttt agccacaaaa cctaggtctg tcccttcggg taaatgagcg ttgatttcag 360  
 caagatcaat ctcagcataa ctgaaatgac tgacgagtaa actacatata agtatcgttc 420  
 gtttgaaaag gcgtaaaagc gtggcagtaa aaaaagaaga tattttatatac ataattgggt 480  
 cgagcagttg ctattttttt attgtcgaac aataatagta tttgaaccct cgagagtaaa 540  
 tcctttttctc gttaaactac tattttttta ttcaactacg gcattgtttt tacaatgttg 600



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tggttttgtt tttatctaaa aaggaagaaa aaacgatt atg aaa cag att cca atg 656
                                     Met Lys Gln Ile Pro Met
                                     1           5

act ata cgt ggt gcg gaa caa tta aga caa gaa ctc gat ttt ttg aaa 704
Thr Ile Arg Gly Ala Glu Gln Leu Arg Gln Glu Leu Asp Phe Leu Lys
          10          15          20

aac act cgt cgc cca gaa att att aat gct atc gca gaa gct cgt gaa 752
Asn Thr Arg Arg Pro Glu Ile Ile Asn Ala Ile Ala Glu Ala Arg Glu
          25          30          35

cat ggc gat cta aaa gaa aat gca gaa tac cat gct gcg cgt gaa cag 800
His Gly Asp Leu Lys Glu Asn Ala Glu Tyr His Ala Ala Arg Glu Gln
          40          45          50

caa gga ttt tgt gaa gga cga atc caa gaa att gaa ggg aaa tta gcg 848
Gln Gly Phe Cys Glu Glu Arg Ile Gln Glu Ile Glu Gly Lys Leu Ala
          55          60          65          70

aat agt caa att att gat gtc aca aag atc cca aat aat ggc aaa gtg 896
Asn Ser Gln Ile Ile Asp Val Thr Lys Ile Pro Asn Asn Gly Lys Val
          75          80          85

att ttt ggt gcc aca att ttg tta ctg aat att gac acg gaa gaa gaa 944
Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn Ile Asp Thr Glu Glu Glu
          90          95          100

gtc tcg tac caa att gta ggc gat gat gaa gcc aat att aaa gca ggg 992
Val Ser Tyr Gln Ile Val Gly Asp Asp Glu Ala Asn Ile Lys Ala Gly
          105          110          115

cta att tca gtt aac gcc acg cga ttg aat tagagaaagc taaatggatt 1042
Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
          120          125

gcccaagatc ttggcgtcaa acaaacgtta attgacactt ccgtcattaa agcgattacg 1102

caaaatgcct taatggacga acaggcaaga attgagcaac atggcagtac accgaatact 1162

ttcgttga 1170

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<210> 22  
 <211> 128  
 <212> PRT  
 <213> Pasteurella multocida

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<400> 22
Met Lys Gln Ile Pro Met Thr Ile Arg Gly Ala Glu Gln Leu Arg Gln
 1           5           10          15

Glu Leu Asp Phe Leu Lys Asn Thr Arg Arg Pro Glu Ile Ile Asn Ala
 20          25          30

Ile Ala Glu Ala Arg Glu His Gly Asp Leu Lys Glu Asn Ala Glu Tyr
 35          40          45

His Ala Ala Arg Glu Gln Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu
 50          55          60

Ile Glu Gly Lys Leu Ala Asn Ser Gln Ile Ile Asp Val Thr Lys Ile
 65          70          75          80

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Pro Asn Asn Gly Lys Val Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn
      85              90              95
Ile Asp Thr Glu Glu Glu Val Ser Tyr Gln Ile Val Gly Asp Asp Glu
      100              105              110
Ala Asn Ile Lys Ala Gly Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
      115              120              125

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<210> 23
<211> 4666
<212> DNA
<213> Pasteurella multocida

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<222> (980) .. (2440)

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<220>
<223> guaB

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gcgatcaatt tattccgata aatcggttgt aatacttcaa tcagctctgc ccaagggtga 180
tcaatttgct gtgtttgttt tgggaaagac aaattaatgc caaagccaat cacgagatta 240
tgttgattat tctgacgatt ggcgatttcg accaaaatcc ctgctaattt gcgcccatgt 300
aatagcacat catttggtcca ttttaatcca atgttcaaag cacctgcttg ctttagcggt 360
tctgcgattg ccatacccac tactaaactc aagccttcta aattgacctt ttggtcacat 420
gccaataaca aactcataat cacttggtcca gcaaaaggag aaagccattg acgaccacgt 480
cgtccacgtc ccgcagtttg atattctgct aagcaaatac cgcccttttc caaatgtgca 540
atattgtcaa gcaagaattg attggctgag ttaataatcg gcttaatata aagtgggtaa 600
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aaatgttgga cttgctgttc tatttgtatc ccttggttgt tcaatttttc gatattgtgt 720
aagatatctt gttctgaata acctaaaagt gcagtcaatt ctgctaaaga aagttgttga 780
tagctagcga gtaatgcaag tacgttttgc ataaaaatcc ttatttatat aaccaaagag 840
aggcaactta ttatagacaa tgattttctc gaaaatcgat aaaaaaatcc attttcaaac 900
agcaacgaaa tctgtataat gcgaccgcaa ttttttttac ccttttatat tccatatcaa 960
cctaagagag aatattgca atg tta cga gta ata aaa gaa gca tta acc ttc 1012
      Met Leu Arg Val Ile Lys Glu Ala Leu Thr Phe
      1              5              10
gat gat gtt ttg ctt gtc cca gca cat tct act gtg ctc cca aat acc 1060
Asp Asp Val Leu Leu Val Pro Ala His Ser Thr Val Leu Pro Asn Thr
      15              20              25

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gca gac ctt tcc act caa ctc acc aaa act atc cgc ctc aat atc cca	1108
Ala Asp Leu Ser Thr Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro	
30 35 40	
atg tta tcc gcc gcc atg gat acc gtg aca gaa act aaa ctg gca atc	1156
Met Leu Ser Ala Ala Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile	
45 50 55	
tct ctt gca caa gaa ggt ggc atc ggg ttt att cat aaa aat atg tct	1204
Ser Leu Ala Gln Glu Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser	
60 65 70 75	
att gag cgt caa gcg gaa cgt gtc cgc aaa gtg aaa aaa ttt gag agc	1252
Ile Glu Arg Gln Ser Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser	
80 85 90	
ggt att gta tcc gat cct gtc acc gtt tca cca acc tta tct tta gca	1300
Gly Ile Val Ser Asp Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala	
95 100 105	
gaa tta agt gaa tta gtg aag aaa aat ggt ttt gcg agt ttc cct gtt	1348
Glu Leu Ser Glu Leu Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val	
110 115 120	
gtt gat gat gaa aaa aat ctt gtc ggt atc att act ggt cgt gat aca	1396
Val Asp Asp Glu Lys Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr	
125 130 135	
cgc ttt gtc acg gat tta aat aaa aca gtg gcg gac ttt atg acc cct	1444
Arg Phe Val Thr Asp Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro	
140 145 150 155	
aaa gct cgt ctt gtc acg gtg aaa cgc aat gca agt cgc gat gaa att	1492
Lys Ala Arg Leu Val Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile	
160 165 170	
ttt ggt cta atg cat aca cac cgt gta gaa aaa gtc ctt gtt gtc agc	1540
Phe Gly Leu Met His Thr His Arg Val Glu Lys Val Leu Val Val Ser	
175 180 185	
gac gat ttc aaa tta aaa ggc atg atc acc tta aaa gac tac caa aaa	1588
Asp Asp Phe Lys Leu Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys	
190 195 200	
tcc gag caa aaa cca caa gcc tgt aaa gat gaa ttt ggt cgt tta cgt	1636
Ser Glu Gln Lys Pro Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg	
205 210 215	
gtc ggt gct gca gta gga gca gga cct ggt aat gaa gaa cgt att gat	1684
Val Gly Ala Ala Val Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp	
220 225 230 235	
gca tta gtg aaa gca ggg gtc gat gtg tta ttg att gac tca tca cac	1732
Ala Leu Val Lys Ala Gly Val Asp Val Leu Leu Ile Asp Ser Ser His	
240 245 250	
ggt cat tca gaa ggt gtg tta caa cgt gtg cgt gaa act cgt gcg aaa	1780
Gly His Ser Glu Gly Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys	
255 260 265	
tac cca gat ttg cca att gtt gca ggt aat gtg gca acc gct gaa ggc	1828
Tyr Pro Asp Leu Pro Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly	
270 275 280	

gca att gcg ttg gct gat gca ggg gca agt gca gtg aaa gtg ggg att 1876  
 Ala Ile Ala Leu Ala Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile  
 285 290 295

ggt cct ggt tca att tgt aca aca cgt att gtc aca ggc gtg ggc gtt 1924  
 Gly Pro Gly Ser Ile Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val  
 300 305 310 315

cca caa att aca gcg att gcc gat gcg gca gaa gca cta aaa gat cgg 1972  
 Pro Gln Ile Thr Ala Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg  
 320 325 330

ggt att cct gtg att gca gat ggc ggt atc cgt ttc tct ggt gat att 2020  
 Gly Ile Pro Val Ile Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile  
 335 340 345

tcg aaa gcc att gcg gcg ggc gcc tct tgt gtt atg gtg ggt tcc atg 2068  
 Ser Lys Ala Ile Ala Ala Gly Ala Ser Cys Val Met Val Gly Ser Met  
 350 355 360

ttt gca ggt aca gaa gaa gca cca ggt gaa atc gaa ctt tat caa ggt 2116  
 Phe Ala Gly Thr Glu Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly  
 365 370 375

cgt gcc ttt aaa tct tat cga ggt atg gga tcg tta ggt gcg atg agc 2164  
 Arg Ala Phe Lys Ser Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser  
 380 385 390 395

aaa ggc tca agc gac cgc tat ttc cag tcc gat aat gca gct gac aaa 2212  
 Lys Gly Ser Ser Asp Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys  
 400 405 410

tta gta cca gaa ggt att gaa gga cgt att cca tat aaa gga ttc tta 2260  
 Leu Val Pro Glu Gly Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu  
 415 420 425

aaa gaa att atc cat caa caa atg ggt gga ttg cgt tct tgt atg ggc 2308  
 Lys Glu Ile Ile His Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly  
 430 435 440

tta acg ggt tgt gca acc att gat gaa ctc cgt acc aaa gcg cag ttt 2356  
 Leu Thr Gly Cys Ala Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe  
 445 450 455

gtg cgc att agt ggt gca ggg atc caa gaa agc cat gtg cat gat gtg 2404  
 Val Arg Ile Ser Gly Ala Gly Ile Gln Glu Ser His Val His Asp Val  
 460 465 470 475

act atc aca aaa gaa gcc cct aat tat cgt atg ggt taaacattgc 2450  
 Thr Ile Thr Lys Glu Ala Pro Asn Tyr Arg Met Gly  
 480 485

ttaggtgggg attatcccca cctaagttta ttttaaataa caacgttaat agagaagctt 2510

atttttatgt atggcattaa aattaaat gttattaaac tttttctatt aaagttttta 2570

agaaataaat atcgatataa aatcaatatt caacatcatc tcattagtat tgaaggaaaa 2630

tgcggtgagt ttgatttaag ccagctaaac tatgtttatt tggtgaaaga tcctgagata 2690

agaaataatc gactgacact gtacttgaat gattttttca aaattggggg aaattatcat 2750

ggatttactc aaatgtatca gacactatca tccaagtatg gttttgatga cgcaacgttt 2810

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cgtataggca gcttagaaaa agtgtccgcg ctacggttaa tccccgtaag cgttga 4666

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<210> 24  
 <211> 487  
 <212> PRT  
 <213> Pasteurella multocida

<400> 24

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Met Leu Arg Val Ile Lys Glu Ala Leu Thr Phe Asp Asp Val Leu Leu
 1           5           10           15

Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr
           20           25           30

Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala
 35           40           45

Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu
 50           55           60

Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala
 65           70           75           80

Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Asp
           85           90           95

Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala Glu Leu Ser Glu Leu
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Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val Val Asp Asp Glu Lys
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Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp
           130          135          140

Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro Lys Ala Arg Leu Val
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Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile Phe Gly Leu Met His
           165          170          175

Thr His Arg Val Glu Lys Val Leu Val Val Ser Asp Asp Phe Lys Leu
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Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ser Glu Gln Lys Pro
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Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val
           210          215          220

Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala
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Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly
           245          250          255

Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro
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Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala
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Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile
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Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala  
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 Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg Gly Ile Pro Val Ile  
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 Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu  
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 Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser  
 370 375 380  
 Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp  
 385 390 395 400  
 Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly  
 405 410 415  
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 gagataaaaa atg gcg aag aaa aag aaa aaa tta caa caa gcg aaa aaa 229  
 Met Ala Lys Lys Lys Lys Lys Leu Gln Gln Ala Lys Lys  
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 Val Gln Val Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu  
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Thr Gly Arg Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala	
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aag tta aaa ggg att tta gaa gat gct gaa ggt ggt gat att acc gcg	373
Lys Leu Lys Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala	
50 55 60	
caa cat gag ctt ttc atg gat att gaa gaa cgc gac agt tgc atc ggg	421
Gln His Glu Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly	
65 70 75	
gca aat att caa acc cgt aag cgt gcg att tta acc ctt gac tgg cgc	469
Ala Asn Ile Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg	
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att gca gag cca cgt aat gcc aca ccg caa gaa gaa aaa ctg caa gtc	517
Ile Ala Glu Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val	
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Glu Ile Asp Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met	
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Val Asp Met Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile	
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Glu Trp Lys Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala	
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cgt ccg cag tcg tgg ttt aaa cta gac aag gat gat aat tta ctg ctt	709
Arg Pro Gln Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu	
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aaa acg cca gat aat caa gac ggt gag ccg ttg aga caa tat ggc tgg	757
Lys Thr Pro Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp	
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Val Val His Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly	
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Leu Phe Arg Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val	
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His Asp Phe Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile	
225 230 235	
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Gly Lys Tyr Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu	
240 245 250	
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Arg Ala Leu Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu	
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Gly Met Asn Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala	
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Ala Arg Leu Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys	
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Thr Ser Thr Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp	
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Ile Ile Leu Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro	
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Ser Arg Val Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu	
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Ser Val Leu Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg	
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415 420 425	
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Leu Asn Asp Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln	
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Asn His Val Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu	
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Ser Ala Asn Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly	
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Leu Ala Gln Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro	
480 485 490	
atg gta aag aaa gct gtt gcg gta ctc atg gca tgt gac tct tac gat	1717
Met Val Lys Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp	
495 500 505	
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Glu Ala Ala Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His	
510 515 520 525	
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Glu His Glu Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu	
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 aaaaaagact tggtaagtga gtttgagaaa aaaggctggg tattcgggca tgataaatct 2108  
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 Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala Gln His Glu  
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 65 70 75 80  
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 85 90 95  
 Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val Glu Ile Asp  
 100 105 110  
 Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met Val Asp Met  
 115 120 125  
 Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile Glu Trp Lys  
 130 135 140  
 Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala Arg Pro Gln  
 145 150 155 160  
 Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu Lys Thr Pro  
 165 170 175

Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp Val Val His  
 180 185 190  
 Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly Leu Phe Arg  
 195 200 205  
 Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val His Asp Phe  
 210 215 220  
 Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile Gly Lys Tyr  
 225 230 235 240  
 Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu Arg Ala Leu  
 245 250 255  
 Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu Gly Met Asn  
 260 265 270  
 Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala Gly Ser Asn  
 275 280 285  
 Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala Ala Arg Leu  
 290 295 300  
 Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys Thr Ser Thr  
 305 310 315 320  
 Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp Leu Leu Val  
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 Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln Ile Ile Leu  
 340 345 350  
 Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro Ser Arg Val  
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 Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu Ser Val Leu  
 370 375 380  
 Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg Ile Pro Glu  
 385 390 395 400  
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 405 410 415  
 Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp Leu Asn Asp  
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 435 440 445  
 Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu Ser Ala Asn  
 450 455 460  
 Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly Leu Ala Gln  
 465 470 475 480  
 Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro Met Val Lys  
 485 490 495  
 Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp Glu Ala Ala  
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Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His Glu His Glu  
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ttt tta gaa gat cgc cgt gaa aag aag ctt acc gaa gaa aaa aca tta 97  
 Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu  
 20 25 30

ggg ctt agt gat gca gtg cgt ttt gct aat gat caa acc cct tat ctc 145  
 Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu  
 35 40 45

cgt tat ggt att gaa tat cga tat aac ggc ttg tct tgg ttg gaa acg 193  
 Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr  
 50 55 60

gta aag ctt ttt ttg gca aag cag aaa atc gaa caa cgt tct gct ctc 241  
 Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu  
 65 70 75 80

caa gag ttt gat att aat aat agg aat aaa ttg gat tcg act atg tcg	289
Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser	
85 90 95	
ttt gta tat tta caa aga cag aat ata gct cgg gga gaa ttt tca acg	337
Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr	
100 105 110	
agt cct tta tat tgg ggg ccg agt cgc cat cgt tta tnt gcg aaa ttc	385
Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe	
115 120 125	
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Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe	
130 135 140	
cgg ccg tgg caa atc aat ana ttc aga caa caa ggt cga aat aac tat	481
Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr	
145 150 155 160	
aca gaa gtg ttt ccc gtt aaa tcc cga gag ttt tct ttt tct ctt atg	529
Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met	
165 170 175	
gac gac att aag att ggc gaa ttg cta cat ctc gga ttg ggc ggt cgg	577
Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Arg	
180 185 190	
tgg gat cac tat aac tat aag cca tta tta aat tct cag cat aat atc	625
Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile	
195 200 205	
aac agg aca cag aga tta cct tat cca aaa aca tca tcc aaa ttt tcg	673
Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser	
210 215 220	
tat caa ttg agt tta gag tat caa tta cat cca tca cat caa att gca	721
Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala	
225 230 235 240	
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Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr	
245 250 255	
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Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp	
260 265 270	
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Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln	
275 280 285	
aat caa tat gcc cat ttc agc gtc ggg ctt ttc cgt aca cgt tat cat	913
Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His	
290 295 300	
aac ttt att caa gaa cgt gag atg acc tgt gat aaa att cca tat gag	961
Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu	
305 310 315 320	
tat aat agg act tat gga tat tgc acg cat aat act tat gta atg ttt	1009
Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe	
325 330 335	

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aaa ggg agc tac agc aaa ggt caa aat cat gac ggc gat ccg tta aaa 1153
Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys
      370              375              380

tct att caa cca tgg aca gtg gta acc ggt att gat tac gaa act gaa 1201
Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu
      385              390              395              400

ggg tgg agc gtg agt ttg agc ggg cgt tat agt gcg gct aaa aaa gcc 1249
Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala
      405              410              415

aaa gat gcg ata gaa acg gaa tac aca cat gat aaa aag gtt gtc aaa 1297
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caa tgg ccg cat tta agt cca tcc tac ttt gtt gtt gat ttt acg ggg 1345
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 Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr  
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 Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu  
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 Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser  
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 Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe  
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 Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr  
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 Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met  
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 Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg  
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 Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile  
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 Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala  
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 Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr  
                     245                    250                    255  
 Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp  
                     260                    265                    270  
 Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln  
                     275                    280                    285  
 Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His  
                     290                    295                    300  
 Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu  
                     305                    310                    315                    320  
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Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu  
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 Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala  
                                   405                                  410                                  415  
 Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys  
                                   420                                  425                                  430  
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 Gln Val  
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gagat	gat	t	tgg	acaaaa	aaa	agcc	ctt	tca	agaa	aga	cgaa	agg	ggc	aaa	atatatt	780		
tgg	agtcata	ct	tttt	tagg	t	atgt	gtc	gg	attata	caca	caaaa	ata	ac	aat	gcaaca	840		
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gta	ataaaa	ag	tg	cggtg	gg	t	ttag	aaa	ag	ttt	g	aat	g			1020		
ttgt	gaaata	cca	agtag	ta	gt	tttt	ta	ag	t	at	at	gat	g	aa		1080		
ccgt	t	aaata	acca	agag	gt	gga	ag	atg	Met	Thr	Glu	Glu	Asn	Lys	Gly	Lys	Arg	1132
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tat	ttt	tta	tgg	ttc	ata	ttg	ttt	atc	ctt	tca	atc	tat	tta	ttt	att			1180
Tyr	Phe	Leu	Trp	Phe	Ile	Leu	Phe	Ile	Leu	Ser	Ile	Tyr	Leu	Phe	Ile			
	10				15					20					25			
acc	ata	caa	gaa	aga	cga	gg	t	tat	tgt	ttt	gac	aaa	cgt	gca	tat	att		1228
Thr	Ile	Gln	Glu	Arg	Arg	Gly	Tyr	Cys	Phe	Asp	Lys	Arg	Ala	Tyr	Ile			
					30				35					40				

cat gag ctt tat act gag caa gag tta att gat cgg ggg att gaa tat 1276  
 His Glu Leu Tyr Thr Glu Gln Glu Leu Ile Asp Arg Gly Ile Glu Tyr  
                     45                    50                    55

gtg gta tcc acc atg ccg tca ggt gtt att aaa cca gat ggc aca ata 1324  
 Val Val Ser Thr Met Pro Ser Gly Val Ile Lys Pro Asp Gly Thr Ile  
                     60                    65                    70

aaa gaa gta aag cgt tac acg agt gtc gag gag ttt aaa cag atg aac 1372  
 Lys Glu Val Lys Arg Tyr Thr Ser Val Glu Glu Phe Lys Gln Met Asn  
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cca gct tgt tgt aca tta acc acc ttt att gat gaa gga ggc gat ggc 1420  
 Pro Ala Cys Cys Thr Leu Thr Thr Phe Ile Asp Glu Gly Gly Asp Gly  
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tat cca gat gat gat gga tat ggt tat gtc aga att gaa tat tta aga 1468  
 Tyr Pro Asp Asp Asp Gly Tyr Gly Tyr Val Arg Ile Glu Tyr Leu Arg  
                     110                    115                    120

cat tat gtt gag aat cta aaa cct tat cat aga gtg att tat ctt gaa 1516  
 His Tyr Val Glu Asn Leu Lys Pro Tyr His Arg Val Ile Tyr Leu Glu  
                     125                    130                    135

tat acg ccc tgt gga gag tta agg gaa gag gcg gct ttt tca aaa aat 1564  
 Tyr Thr Pro Cys Gly Glu Leu Arg Glu Glu Ala Ala Phe Ser Lys Asn  
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 acaaattctt gaaaaaggag atgaacattt cgaagtaaat tttaattgat caaagtactc 2344  
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 20 25 30  
 Tyr Cys Phe Asp Lys Arg Ala Tyr Ile His Glu Leu Tyr Thr Glu Gln  
 35 40 45  
 Glu Leu Ile Asp Arg Gly Ile Glu Tyr Val Val Ser Thr Met Pro Ser  
 50 55 60  
 Gly Val Ile Lys Pro Asp Gly Thr Ile Lys Glu Val Lys Arg Tyr Thr  
 65 70 75 80  
 Ser Val Glu Glu Phe Lys Gln Met Asn Pro Ala Cys Cys Thr Leu Thr  
 85 90 95  
 Thr Phe Ile Asp Glu Gly Gly Asp Gly Tyr Pro Asp Asp Asp Gly Tyr  
 100 105 110  
 Gly Tyr Val Arg Ile Glu Tyr Leu Arg His Tyr Val Glu Asn Leu Lys  
 115 120 125  
 Pro Tyr His Arg Val Ile Tyr Leu Glu Tyr Thr Pro Cys Gly Glu Leu  
 130 135 140  
 Arg Glu Glu Ala Ala Phe Ser Lys Asn  
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gcagaactgg ctagcttata acttttagat aattgtatta ttaaaagaag ctgtatgatt 180

gttattctat cattagtga taataaatat tctttatttt ttgagagata aaaacaattc 240

atatttcaat agaaaacaga aaataaagat tatcaaaaga attatccgctc cttataaata 300

tgagtctgta ttgtgagatg atat atg aat att tta ttt gtt tct gat gat 351
                        Met Asn Ile Leu Phe Val Ser Asp Asp
                          1                      5

gtt tat gct aaa cat ctg gtg gtt gcg att aaa agc att ata aat cat 399
Val Tyr Ala Lys His Leu Val Val Ala Ile Lys Ser Ile Ile Asn His
 10                      15                      20                      25

aat gaa aaa ggt att tca ttt tat att ttt gat ttg ggt ata aag gat 447
Asn Glu Lys Gly Ile Ser Phe Tyr Ile Phe Asp Leu Gly Ile Lys Asp
          30                      35                      40

gaa aat aag aga aat att aat gat att gtt tct tct tat gga agt gaa 495
Glu Asn Lys Arg Asn Ile Asn Asp Ile Val Ser Ser Tyr Gly Ser Glu
          45                      50                      55

gtc aac ttt att gct gtg aat gag aaa gaa ttt gag agt ttt cct gtt 543
Val Asn Phe Ile Ala Val Asn Glu Lys Glu Phe Glu Ser Phe Pro Val
          60                      65                      70

caa att agt tat att tct tta gca aca tat gca agg cta aaa gcg gca 591
Gln Ile Ser Tyr Ile Ser Leu Ala Thr Tyr Ala Arg Leu Lys Ala Ala
          75                      80                      85

gag tat ttg ccg gat aat tta aat aaa att att tat tta gat gtt gat 639
Glu Tyr Leu Pro Asp Asn Leu Asn Lys Ile Ile Tyr Leu Asp Val Asp
          90                      95                      100                      105

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gtt ttg gtt ttt aac tca tta gaa atg tta tgg aat gtt gat gtt aat 687  
 Val Leu Val Phe Asn Ser Leu Glu Met Leu Trp Asn Val Asp Val Asn  
 110 115 120

aat ttt ctt acc gca gcc tgt tat gat tct ttc atc gaa aat gaa aag 735  
 Asn Phe Leu Thr Ala Ala Cys Tyr Asp Ser Phe Ile Glu Asn Glu Lys  
 125 130 135

tct gag cat aaa aaa tcg att tca atg tca gat aag gaa tat tat ttt 783  
 Ser Glu His Lys Lys Ser Ile Ser Met Ser Asp Lys Glu Tyr Tyr Phe  
 140 145 150

aat gca gga gta atg cta ttt aat tta gat gaa tgg cgg aag atg gat 831  
 Asn Ala Gly Val Met Leu Phe Asn Leu Asp Glu Trp Arg Lys Met Asp  
 155 160 165

gta ttc tca aga gct tta gac ctg tta gct atg tat cct aat caa atg 879  
 Val Phe Ser Arg Ala Leu Asp Leu Leu Ala Met Tyr Pro Asn Gln Met  
 170 175 180 185

att tat cag gat caa gat ata ttg aat atc ctt ttt agg aat aaa gtc 927  
 Ile Tyr Gln Asp Gln Asp Ile Leu Asn Ile Leu Phe Arg Asn Lys Val  
 190 195 200

tgt tat tta gat tgc aga ttt aat ttc atg cca aat caa ctt gaa aga 975  
 Cys Tyr Leu Asp Cys Arg Phe Asn Phe Met Pro Asn Gln Leu Glu Arg  
 205 210 215

ata aan caa tac cat aaa gga aaa ntg agc aac tta cat tct tta gaa 1023  
 Ile Xaa Gln Tyr His Lys Gly Lys Xaa Ser Asn Leu His Ser Leu Glu  
 220 225 230

aaa aca acg atg cct gtc gtt att tca cat tat tgt ggt cca gaa aaa 1071  
 Lys Thr Thr Met Pro Val Val Ile Ser His Tyr Cys Gly Pro Glu Lys  
 235 240 245

gcg tgg cat gcg gat tgt aaa cat ttt aat gta tat ttc tat cag aaa 1119  
 Ala Trp His Ala Asp Cys Lys His Phe Asn Val Tyr Phe Tyr Gln Lys  
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 Ile Leu Ala Xaa Ser Arg Gly Xaa Asp Lys Glu Arg Val Leu Ser  
 270 275 280

ata aaa act tat ctc aag gcc ttg att aga agg att aga tat aaa ttc 1215  
 Ile Lys Thr Tyr Leu Lys Ala Leu Ile Arg Arg Ile Arg Tyr Lys Phe  
 285 290 295

aaa tat caa gtc tat taactattga atttttgcaa atgagataag agtatagtgc 1270  
 Lys Tyr Gln Val Tyr  
 300

tgattttcttc aaagcgaaaa ggaggaaata gcttggttcta atttattaca ataatgggtg 1330

tattcatctt gattttgaag gaaagagagt gttttttgta taaaagcatt ttcgtcacct 1390

aaatttacta atcctccaaa ttctcctcct cgnagaattt ctttcggacc ggtagggcag 1450

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tctttcaaag aggtgtgtaa aaatagctta gcatttttta ttaatggata cggattatct 1570

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           20                  25                  30  
 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn  
       35                  40                  45  
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn  
       50                  55                  60  
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu  
       65                  70                  75                  80  
 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu  
           85                  90                  95  
 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu  
       100                  105                  110  
 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys  
       115                  120                  125  
 Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile  
       130                  135                  140

Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe  
 145 150 155 160  
 Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp  
 165 170 175  
 Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile  
 180 185 190  
 Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe  
 195 200 205  
 Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Xaa Gln Tyr His Lys Gly  
 210 215 220  
 Lys Xaa Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val  
 225 230 235 240  
 Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys  
 245 250 255  
 His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Xaa Xaa Ser Arg  
 260 265 270  
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 275 280 285  
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 1 5 10 15  
 gga cac cca gat gca gaa gct cgt aca aaa ttc gtc att aaa gaa tta 97  
 Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu  
 20 25 30  
 nat aat aaa ggc att caa gat gag caa tta ttc atc gac acg ggg atg 145  
 Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met  
 35 40 45  
 tgg gat gcc gct tta gcg aaa gat aaa atg gat gca tgg tta tct agc 193  
 Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser  
 50 55 60  
 tct aaa gca aat caa att gaa gtg atc atc gct aac aac gat ggt atg 241  
 Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met  
 65 70 75 80  
 gcg atg ggg gca ttg gaa gcc acg aaa gca cat ggt aaa aaa tta cca 289  
 Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro  
 85 90 95  
 atc ttc ngg gta nat gcg tta cca gaa gtc ctc caa tta atc aaa aaa 337  
 Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys  
 100 105 110  
 ggt gaa att gca ggt acg gtg tta aat gac ggt gtg aac caa ggt aaa 385  
 Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys  
 115 120 125  
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 Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr  
 130 135 140



gaa ggc aca aaa tgg cag tta aaa cga tgg tgt cct acg tat ccc tta 481  
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 Cys Trp Cys Gly Cys Gly  
 165

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Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
          35           40           45
Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
          50           55           60
Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
          65           70           75           80
Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
          85           90           95
Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
          100          105          110
Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
          115          120          125
Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
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Cys Trp Cys Gly Cys Gly
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attacgcagt gaaaatgaac aactaaagag tgagcaccaa aactggcaag aacgtttacg 240
ctcattatta ggcaaaattg ataacgtata attcacttct tattaaggct tagtttttct 300
aagccttatt ttttaggaga aatta atg aaa aca aaa att tgt att atc act 352
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Gly Ser Thr Leu Gly Gly Ala Glu Tyr Val Ala Glu His Ile Ala Glu
10                               15                               20                               25

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Ile Leu Glu Gln Gln Asp Tyr Pro Val Arg Leu Glu His Gly Pro Asn
30                               35                               40

ttt gaa gaa gtg atc gat gaa aaa tgt tgg ctt gtt gtc acc tct acc 496
Phe Glu Glu Val Ile Asp Glu Lys Cys Trp Leu Val Val Thr Ser Thr
45                               50                               55

cat ggt gca ggt gaa tta ccg gat aat att aaa cct ctg ttt gaa aaa 544
His Gly Ala Gly Glu Leu Pro Asp Asn Ile Lys Pro Leu Phe Glu Lys
60                               65                               70

tta gca ttt cac cca aaa cag tta gct gac tta cgc ttt gcg gtg atc 592
Leu Ala Phe His Pro Lys Gln Leu Ala Asp Leu Arg Phe Ala Val Ile
75                               80                               85

ggg tta ggt aat tcg gat tat gat acc ttc tgt cac gca gtg gat cat 640
Gly Leu Gly Asn Ser Asp Tyr Asp Thr Phe Cys His Ala Val Asp His
90                               95                               100                               105

gtg gaa caa tta ctg cta agc aaa gat gct tta caa ctg tgt gaa tcg 688
Val Glu Gln Leu Leu Leu Ser Lys Asp Ala Leu Gln Leu Cys Glu Ser
110                               115                               120

cta aga atg gat atg cta acc att act gat cct gaa cac acg gcc gaa 736
Leu Arg Met Asp Met Leu Thr Ile Thr Asp Pro Glu His Thr Ala Glu
125                               130                               135

caa tgg ctc cca caa ttt ctc agt caa tta taatatttat tccctataca 786
Gln Trp Leu Pro Gln Phe Leu Ser Gln Leu
140                               145

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&lt;210&gt; 40

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 40

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Glu Tyr Val Ala Glu His Ile Ala Glu Ile Leu Glu Gln Gln Asp Tyr
          20             25             30

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Pro Val Arg Leu Glu His Gly Pro Asn Phe Glu Glu Val Ile Asp Glu
      35             40             45

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Lys Cys Trp Leu Val Val Thr Ser Thr His Gly Ala Gly Glu Leu Pro  
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 Asp Asn Ile Lys Pro Leu Phe Glu Lys Leu Ala Phe His Pro Lys Gln  
     65                    70                    75                    80  
 Leu Ala Asp Leu Arg Phe Ala Val Ile Gly Leu Gly Asn Ser Asp Tyr  
                     85                    90                    95  
 Asp Thr Phe Cys His Ala Val Asp His Val Glu Gln Leu Leu Leu Ser  
             100                    105                    110  
 Lys Asp Ala Leu Gln Leu Cys Glu Ser Leu Arg Met Asp Met Leu Thr  
             115                    120                    125  
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 Ser Gln Leu  
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                          1             5             10

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Ser Asn Asp Leu Ser Ile Asp Leu Gly Thr Ala Asn Thr Leu Ile Tyr
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gtc aaa gga caa ggg att gtt tta gat gaa cct tct gtt gtg gcg att 3328
Val Lys Gly Gln Gly Ile Val Leu Asp Glu Pro Ser Val Val Ala Ile
                        30             35             40

cgc caa gaa cgt tca ggt gca tta aaa agc att gct gcg gtt ggt cgt 3376
Arg Gln Glu Arg Ser Gly Ala Leu Lys Ser Ile Ala Ala Val Gly Arg
                        45             50             55

gat gcc aaa tta atg tta ggc cgt aca ccg aaa agc att gca gcg att 3424
Asp Ala Lys Leu Met Leu Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile
                        60             65             70

cgt cct atg aaa gat ggg gtg atc gca gat ttc ttt gtg aca gaa aaa 3472
Arg Pro Met Lys Asp Gly Val Ile Ala Asp Phe Phe Val Thr Glu Lys
                        75             80             85             90

atg ttg caa tat ttt att aaa caa gtg cac agc agc aat ttt atg cgt 3520
Met Leu Gln Tyr Phe Ile Lys Gln Val His Ser Ser Asn Phe Met Arg
                        95             100             105

cca agt cca cgt gtc tta gtt tgt gta cct gcg gga gct acg caa gtc 3568
Pro Ser Pro Arg Val Leu Val Cys Val Pro Ala Gly Ala Thr Gln Val
                        110             115             120

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Glu Arg Arg Ala Ile Lys Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu
                        125             130             135

gtg tac ttg att gag gaa ccg atg gcg gca gcg att ggt gct aaa tta 3664
Val Tyr Leu Ile Glu Glu Pro Met Ala Ala Ala Ile Gly Ala Lys Leu
                        140             145             150

cct gtt tcg act gcc aca ggt tcg atg gtg atc gat atc ggt ggt ggt 3712
Pro Val Ser Thr Ala Thr Gly Ser Met Val Ile Asp Ile Gly Gly Gly
                        155             160             165             170

acg acg gaa gtt gcg gtg att tct tta aat ggc att gtg tat tcc tct 3760
Thr Thr Glu Val Ala Val Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser
                        175             180             185

tca gtc cgc att ggt ggt gat cgt ttt gat gag gcg att att tct tat 3808

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Ser Val Arg Ile Gly Gly Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr	
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Val Arg Lys Thr Phe Gly Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg	
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Ile Lys Gln Glu Ile Gly Ser Ala Phe Ile Gln Glu Gly Asp Glu Val	
220 225 230	
cgt gaa att gaa gtg cat ggt cat aac tta gca gaa ggt gcg ccg cgt	3952
Arg Glu Ile Glu Val His Gly His Asn Leu Ala Glu Gly Ala Pro Arg	
235 240 245 250	
tct ttc aaa ctc acc tca cgt gat gtg tta gaa gct att caa gcc ccg	4000
Ser Phe Lys Leu Thr Ser Arg Asp Val Leu Glu Ala Ile Gln Ala Pro	
255 260 265	
tta aat ggc att gtt gcg gca gtg cgc acg gcc ttg gaa gag tgt caa	4048
Leu Asn Gly Ile Val Ala Ala Val Arg Thr Ala Leu Glu Glu Cys Gln	
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Pro Glu His Ala Ala Asp Ile Phe Glu Arg Gly Met Val Leu Thr Gly	
285 290 295	
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Gly Gly Ala Leu Ile Arg Asn Ile Asp Val Leu Ser Lys Glu Thr	
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<210> 42

<211> 351

<212> PRT

<213> Pasteurella multocida

<400> 42

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 Val Leu Asp Glu Pro Ser Val Val Ala Ile Arg Gln Glu Arg Ser Gly  
 35 40 45  
 Ala Leu Lys Ser Ile Ala Ala Val Gly Arg Asp Ala Lys Leu Met Leu  
 50 55 60  
 Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile Arg Pro Met Lys Asp Gly  
 65 70 75 80  
 Val Ile Ala Asp Phe Phe Val Thr Glu Lys Met Leu Gln Tyr Phe Ile  
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 Lys Gln Val His Ser Ser Asn Phe Met Arg Pro Ser Pro Arg Val Leu  
 100 105 110  
 Val Cys Val Pro Ala Gly Ala Thr Gln Val Glu Arg Arg Ala Ile Lys  
 115 120 125  
 Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu Val Tyr Leu Ile Glu Glu  
 130 135 140  
 Pro Met Ala Ala Ala Ile Gly Ala Lys Leu Pro Val Ser Thr Ala Thr  
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 Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr Val Arg Lys Thr Phe Gly  
 195 200 205  
 Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg Ile Lys Gln Glu Ile Gly  
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 Ser Ala Phe Ile Gln Glu Gly Asp Glu Val Arg Glu Ile Glu Val His  
 225 230 235 240  
 Gly His Asn Leu Ala Glu Gly Ala Pro Arg Ser Phe Lys Leu Thr Ser

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Ile Phe Glu Arg Gly Met Val Leu Thr Gly Gly Gly Ala Leu Ile Arg
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Asn Ile Asp Val Leu Leu Ser Lys Glu Thr Gly Val Pro Val Ile Ile
                305                310                315                320
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&lt;210&gt; 43

&lt;211&gt; 2172

&lt;212&gt; DNA

&lt;213&gt; Pasteurella multocida

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&lt;222&gt; (1)..(1464)

&lt;220&gt;

&lt;223&gt; pnp

&lt;400&gt; 43

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Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg
                20                25                30

atc act gaa aac aag cac gtt atg aac aaa att gat gcg att aaa gct      144
Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala
                35                40                45

gat gtg att gca caa atc aca gct gaa gta gca gaa ggc gaa gac atc      192
Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile
   50                55                60

agt gaa ggg aaa att gtc gat att ttc acc gca ctt gaa agc caa atc      240
Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile
   65                70                75                80

gta cgt agc cgt atc att gct ggt gaa cca cgt att gat ggt cgt aca      288
Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr
                85                90                95

gtg gat act gtt cgt gca tta gat att tgt act ggt gtt tta cca cgt      336
Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg
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aca cac ggt tct gcg att ttc acc cgt ggt gaa aca cag gcg tta gct      384

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Val	Ala	Thr	Leu	Gly	Thr	Glu	Arg	Asp	Ala	Gln	Ile	Ile	Asp	Glu	Leu		
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Tyr	Ser	Val	Gly	Glu	Thr	Gly	Met	Ile	Gly	Ser	Pro	Lys	Arg	Arg	Glu		
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Thr	Leu	Ala	Glu	Phe	Pro	Tyr	Val	Val	Arg	Val	Val	Ser	Glu	Ile	Thr		
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Ala	Leu	Met	Asp	Ala	Gly	Val	Pro	Ile	Lys	Ala	Ala	Val	Ala	Gly	Ile		
		225			230				235						240		
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Ile	Leu	Gly	Asp	Glu	Asp	His	Leu	Gly	Asp	Met	Asp	Phe	Lys	Val	Ala		
			260					265					270				
ggc	aca	cgt	acg	ggc	gtg	acg	gca	tta	caa	atg	gat	atc	aaa	atc	gaa	864	
Gly	Thr	Arg	Thr	Gly	Val	Thr	Ala	Leu	Gln	Met	Asp	Ile	Lys	Ile	Glu		
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ggc	atc	aca	gca	gaa	atc	atg	caa	att	gcg	tta	aac	caa	gcg	aaa	agc	912	
Gly	Ile	Thr	Ala	Glu	Ile	Met	Gln	Ile	Ala	Leu	Asn	Gln	Ala	Lys	Ser		
		290				295					300						
gca	cgt	tta	cac	att	tta	ggc	gtg	atg	gag	caa	gcg	atc	cca	gcg	cca	960	
Ala	Arg	Leu	His	Ile	Leu	Gly	Val	Met	Glu	Gln	Ala	Ile	Pro	Ala	Pro		
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Arg	Ala	Asp	Ile	Ser	Asp	Phe	Ala	Pro	Arg	Ile	Tyr	Thr	Met	Lys	Ile		
				325					330						335		
gat	ccg	aag	aaa	atc	aaa	gat	gtg	atc	ggc	aaa	ggc	ggc	gca	acc	att	1056	
Asp	Pro	Lys	Lys	Ile	Lys	Asp	Val	Ile	Gly	Lys	Gly	Gly	Ala	Thr	Ile		
			340				345						350				
cgt	gcc	tta	aca	gaa	gaa	aca	ggc	acc	tca	att	gat	atc	gat	gat	gat	1104	
Arg	Ala	Leu	Thr	Glu	Glu	Thr	Gly	Thr	Ser	Ile	Asp	Ile	Asp	Asp	Asp		
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370 375 380

atg gcg cgt att gaa gat att act gca gaa gtt gaa gcg ggt gca gtg 1200
Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val
385 390 395 400

tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt gcc ttc gtt tct 1248
Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser
405 410 415

atc gta ggt aac aaa gaa ggc tta gtg cat att tct caa atc gcg gaa 1296
Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu
420 425 430

gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg ggg caa gaa gtg 1344
Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
435 440 445

act gtt aaa gtg gtt gag att gat cgt caa ggt cgt att cgt tta acc 1392
Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
450 455 460

atg aaa gaa gtt gca cca aag caa gaa cac gtt gat tct gtt gtc gca 1440
Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala
465 470 475 480

gac gtt gcc gca gaa gaa aac gca taagcaataa acaccaacgc ccttcgtgat 1494
Asp Val Ala Ala Glu Asn Ala
485

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<213> Pasteurella multocida

<400> 44

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 Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr  
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 Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala  
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 Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro Pro  
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 Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu  
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 Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr  
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 Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu  
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 Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile  
 225 230 235 240  
 Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp  
 245 250 255  
 Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala  
 260 265 270  
 Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu  
 275 280 285  
 Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser  
 290 295 300  
 Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro  
 305 310 315 320  
 Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile  
 325 330 335

Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile  
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 Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val  
                   370                  375                  380  
 Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val  
                   385                  390                  395                  400  
 Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser  
                   405                  410                  415  
 Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu  
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 Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val  
                   435                  440                  445  
 Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr  
                   450                  455                  460  
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 <213> Pasteurella multocida

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 ggt gaa aaa att gca cgg gaa tgg gcg gat gtg gat gat att gat gtg 97  
 Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val  
                   20                  25                  30  
  
 gtc att cct gtg cct gaa acc tct aac gat att gct tta cgt att gcg 145  
 Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala  
                   35                  40                  45  
  
 cgc gtg tta aat aaa ccg tat cgt caa ggt ttt gtg aaa aat cgc tat 193  
 Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr  
                   50                  55                  60  
  
 gta gga cgt acg ttt att atg ccg ggg cag gca ttg cga gtc agt tct 241  
 Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser  
                   65                  70                  75                  80

gtt aga cgt aaa ctc aat acc att gct tca gaa ttt aaa gat aag aat 289  
 Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn  
                             85                            90                            95

gtg tta tta gtt gac gac tcg att gta cgt ggt acc acg tct gaa caa 337  
 Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln  
                             100                            105                            110

att gtc gaa atg gcg aga gcg gca ggt gcg aag aaa att tat ttt gcc 385  
 Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala  
                             115                            120                            125

tct gct gca cca gaa att cgt tat cca aat gtg tat ggt att gat atg 433  
 Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met  
                             130                            135                            140

cca acc aaa aat gaa ttg atc gct tat ggt cgt gat gta gat gaa att 481  
 Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile  
                             145                            150                            155                            160

gct aac tta att ggt gtg gat aaa ttg att ttc caa gat ttg gat gcg 529  
 Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala  
                             165                            170                            175

tta act ggt tct gtg caa caa gaa aat cca agt att caa gac ttt gat 577  
 Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp  
                             180                            185                            190

tgt tcg gtg ttt aca ggg gtt tat gtg acg ggc gat att aca cct gaa 625  
 Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu  
                             195                            200                            205

tat ctg ga 633  
 Tyr Leu  
             210

&lt;210&gt; 46

&lt;211&gt; 210

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 46

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Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val  
                             20                            25                            30

Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala  
                             35                            40                            45

Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr  
                             50                            55                            60

Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser  
   65                            70                            75                            80

Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn  
                             85                            90                            95

Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln  
                             100                            105                            110

Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala  
           115                          120                          125  
 Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met  
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 Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile  
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 Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala  
                           165                          170                          175  
 Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp  
                           180                          185                          190  
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 Tyr Leu  
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 att att ttt aga gat gta ata gaa cgc tat caa aat gaa gtg tct ata 96  
 Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile  
           20                          25                          30  
 act aaa aaa ggc gcg cga aat gaa att ata aga tta aac cgc ttt tta 144  
 Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu  
           35                          40                          45  
 aga tat gat att tct aat ctg tat att cgt gat tta aga aaa gaa gat 192  
 Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp  
           50                          55                          60  
 ttt gag gag tgg atc aga att cgc cta acc gaa gta tcg gat gct agc 240  
 Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser  
           65                          70                          75                          80  
 gtt aga cgt gag ctt gtt act ata tcg tca gtg ctg aca aca gca ata 288  
 Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile  
                           85                          90                          95  
 aat aag tgg gga tat att tca agg cat cca atg act ggt att gaa aaa 336



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Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met Thr Gly Ile Glu Lys
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cca aaa aac tcg gca gaa aga aaa gaa cga tat tca gaa cag gac att 384
Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Glu Gln Asp Ile
      115                      120                      125

aaa aca ata tta gaa aca gct aga tat tgt gaa gat aaa cta ccc ata 432
Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile
      130                      135                      140

aca ctc aaa caa aga gta gca att gca atg tta ttt gct att gaa acc 480
Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr
      145                      150                      155                      160

gct atg cgt gct ggt gag att gct agt ata aaa tgg gat aat gtt ttt 528
Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys Trp Asp Asn Val Phe
      165                      170                      175

ctt gaa aag aga ata gta cat tta ccg aca act aaa aac ggg cac tct 576
Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser
      180                      185                      190

aga gat gtg ccg ctt tcg caa aga gct gtt gcg cta att tta aaa atg 624
Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met
      195                      200                      205

aaa gag gta gaa aat gga gat ctt gtg ttt cag acc acg cct gaa tca 672
Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln Thr Thr Pro Glu Ser
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tta agc acc acg ttt aga gtg tta aag aaa gag tgt gga ctt gaa cat 720
Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu Cys Gly Leu Glu His
      225                      230                      235                      240

ctc cat ttt cat gat acg aga agg gaa gcg ttg acg aga tta tct aag 768
Leu His Phe His Asp Thr Arg Arg Glu Ala Leu Thr Arg Leu Ser Lys
      245                      250                      255

aaa gta gat gta atg act cta gcc aaa att agc gga cat aga gat tta 816
Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser Gly His Arg Asp Leu
      260                      265                      270

aga att tta caa aac aca tat tac gca ccg aat atg agt gaa gtg gca 864
Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn Met Ser Glu Val Ala
      275                      280                      285

aac ttg ttg gat taattcactc ttcttaaata cgctttttgc cacttgatta 916
Asn Leu Leu Asp
      290

catcgccagc cttatatctt ttactttcat tacttccttt ttctaatagaa actgggggatg 976

gaaagtcttg gcgggtaata atatgacgag atgtgtaatt gtaagaacga ttaatcatga 1036

tagaaatgtc ttcaatacta agaagaactg gactatcttc ttttaagtga gctaaggctc 1096

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&lt;210&gt; 48

&lt;211&gt; 292

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 48

Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys Gly Ile Ala Pro Asp

1

5

10

15

```

Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile
      20                      25                      30
Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu
      35                      40                      45
Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp
      50                      55                      60
Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser
      65                      70                      75                      80
Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile
      85                      90                      95
Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met Thr Gly Ile Glu Lys
      100                     105                     110
Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Glu Gln Asp Ile
      115                     120                     125
Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile
      130                     135                     140
Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr
      145                     150                     155                     160
Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys Trp Asp Asn Val Phe
      165                     170                     175
Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser
      180                     185                     190
Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met
      195                     200                     205
Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln Thr Thr Pro Glu Ser
      210                     215                     220
Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu Cys Gly Leu Glu His
      225                     230                     235                     240
Leu His Phe His Asp Thr Arg Arg Glu Ala Leu Thr Arg Leu Ser Lys
      245                     250                     255
Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser Gly His Arg Asp Leu
      260                     265                     270
Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn Met Ser Glu Val Ala
      275                     280                     285
Asn Leu Leu Asp
      290

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<210> 49
<211> 1618
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (2)..(1195)

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&lt;220&gt;

&lt;223&gt; sopE

&lt;400&gt; 49

g ggc gat cta tgt ctg aaa ata tct aca tgg tgt caa agt cac aga atc 49  
 Gly Asp Leu Cys Leu Lys Ile Ser Thr Trp Cys Gln Ser His Arg Ile  
 1 5 10 15

aat caa gca att cgc aca att caa agt cta tca acc gca gtc atc ggt 97  
 Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly  
 20 25 30

att gtc tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat 145  
 Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn  
 35 40 45

gaa ccc gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga 193  
 Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly  
 50 55 60

aaa caa ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc 241  
 Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val  
 65 70 75 80

aat tgc aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac 289  
 Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp  
 85 90 95

gaa gaa aca aaa gca agt gaa atg aac acg gca att att ggc aca atc 337  
 Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile  
 100 105 110

aca gaa gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa 385  
 Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys  
 115 120 125

aac aaa ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac 433  
 Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp  
 130 135 140

aca aaa gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac 481  
 Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn  
 145 150 155 160

gca ttt gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg 529  
 Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala  
 165 170 175

gtg caa tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg 577  
 Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met  
 180 185 190

ggc gat ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac 625  
 Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp  
 195 200 205

tat gcc gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa 673  
 Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu  
 210 215 220

cag ggc tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc 721  
 Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser  
 225 230 235 240

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ggt gtc aca caa cca ctc tat ttt gac att aac gac agc tcg act gat 769
Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp
245 250 255

gtg aac tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat 817
Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn
260 265 270

ggc ttt cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc 865
Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe
275 280 285

aag ttt gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att 913
Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile
290 295 300

gca ggg gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta 961
Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu
305 310 315 320

gtg aaa gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc 1009
Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr
325 330 335

aca aaa ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt 1057
Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu
340 345 350

aac agt gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat 1105
Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp
355 360 365

tat cac cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att 1153
Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile
370 375 380

tct gat gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg 1195
Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
385 390 395

taaggggtag aaaatggctt taccacgcaa acttaaattg atgaatttaa tcatcgacgg 1255

taacaaatat ctccggcgaag tcacggaagt gactcaacca aaattagcaa tgaaaatcga 1315

agaatttcgc gcgggcggta tgattggttc ggtggatgtc aatctcgggc ttgaaaagct 1375

cgaagcggaa tttaaagccg gtggctacat ggtcgaatta attaaaaaat tcggcgggtc 1435

aatcaacggc attccattgc gttttcttgg ctcatatcag cgtgatgaca cagaagaagt 1495

cacatctgtt gagcttgtga tgcaaggctcg atttactgaa attgacagcg gaaacagcaa 1555

agtgggcgat gacactgaac aaacattcaa agtgccttta acgtattaca aaatcattgt 1615

tga 1618

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&lt;210&gt; 50

&lt;211&gt; 398

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 50

Gly Asp Leu Cys Leu Lys Ile Ser Thr Trp Cys Gln Ser His Arg Ile  
 1 5 10 15  
 Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly  
 20 25 30  
 Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn  
 35 40 45  
 Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly  
 50 55 60  
 Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val  
 65 70 75 80  
 Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp  
 85 90 95  
 Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile  
 100 105 110  
 Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys  
 115 120 125  
 Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp  
 130 135 140  
 Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn  
 145 150 155 160  
 Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala  
 165 170 175  
 Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met  
 180 185 190  
 Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp  
 195 200 205  
 Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu  
 210 215 220  
 Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser  
 225 230 235 240  
 Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp  
 245 250 255  
 Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn  
 260 265 270  
 Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe  
 275 280 285  
 Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile  
 290 295 300  
 Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu  
 305 310 315 320  
 Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr  
 325 330 335

Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu  
                   340                  345                  350

Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp  
                   355                  360                  365

Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile  
                   370                  375                  380

Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser  
                   385                  390                  395

<210> 51  
 <211> 353  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <221> CDS  
 <222> (1)..(351)

<220>  
 <223> unknown C1

<400> 51  
 atg aca tta ttt gat gaa tgt aaa tta gct ctt aga gac gat ttt aat 48  
 Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn  
       1                  5                  10                  15

cta att tgt gat gaa gag aag gat tgt gta atg gat aag ttt tat ttc 96  
 Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe  
                   20                  25                  30

tat ttc ttg gaa aag aaa gag gaa ttt aat ttt caa gat tat tca ttt 144  
 Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe  
                   35                  40                  45

gaa gaa atg tat ata ttt tca aaa atg gaa cct gtg tat gtt tta tgt 192  
 Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys  
                   50                  55                  60

gat agc tct aat ata cct ttg ttt agg agt aat tgg gaa ttg att atc 240  
 Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile  
                   65                  70                  75                  80

aat aat ata tat gat gtt gtc tgt tta tct aca aaa gta ttt ttt cta 288  
 Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu  
                   85                  90                  95

gat gat gaa aag tta atg atg gaa tta ttt cct gaa gat aaa gta aga 336  
 Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg  
                   100                  105                  110

gtc atc tat aaa aga ta 353  
 Val Ile Tyr Lys Arg  
                   115

<210> 52  
 <211> 117  
 <212> PRT  
 <213> Pasteurella multocida



&lt;400&gt; 52

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Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
 1          5          10          15
Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
          20          25          30
Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
          35          40          45
Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
          50          55          60
Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
          65          70          75          80
Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
          85          90          95
Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
          100          105          110
Val Ile Tyr Lys Arg
          115

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&lt;210&gt; 53

&lt;211&gt; 509

&lt;212&gt; DNA

<213> *Pasteurella multocida*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(507)

&lt;220&gt;

&lt;223&gt; unknown C2

&lt;400&gt; 53

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atg aaa aat ttt agg aat ata aat att tat agt gat tat gga aag gtt 48
Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val
 1          5          10          15
gat aag gaa att ata tta gaa ttc gaa aat gaa ttt aat ata aag ctt 96
Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu
          20          25          30
cct tct tta tac ata gat tta att acg gcg cat aat gct ccg aag agt 144
Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser
          35          40          45
gaa gag aat tgc ttt gaa tat tac aat gag cgt aat gag ccc acg ttt 192
Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe
          50          55          60
tct tcc ttt gga ttt gaa ggg ttt gag aca gag cgg tct agc gcc tct 240
Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser
          65          70          75          80
ctt gaa aat ata tat gct cag tat att tat gat gat cca atc tat ggt 288
Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly
          85          90          95

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tat gaa cat gtg tat tct ttt ggt agt act ggc gag gga cat ttt atc 336  
 Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile  
                   100                  105                  110

tgt ttt gat tat cgt gat gat cca aaa ggt gat gaa ccc aaa atc tgt 384  
 Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys  
                   115                  120                  125

atc gtg att cac gat gaa tat gat gaa aaa aca ggg aaa atg cga ctg 432  
 Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu  
                   130                  135                  140

ttt cct ata gca gag aat ttt gaa gcg ttt tta gat agt ttg aaa tca 480  
 Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser  
                   145                  150                  155                  160

ttt gat gaa atg ata gag aag tat tcg ta 509  
 Phe Asp Glu Met Ile Glu Lys Tyr Ser  
                   165

<210> 54

<211> 169

<212> PRT

<213> Pasteurella multocida

<400> 54

Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val  
           1                  5                  10                  15

Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu  
                   20                  25                  30

Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser  
           35                  40                  45

Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe  
           50                  55                  60

Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser  
           65                  70                  75                  80

Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly  
                   85                  90                  95

Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile  
                   100                  105                  110

Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys  
           115                  120                  125

Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu  
           130                  135                  140

Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser  
           145                  150                  155                  160

Phe Asp Glu Met Ile Glu Lys Tyr Ser  
                   165

<210> 55

<211> 443

&lt;212&gt; DNA

&lt;213&gt; Pasteurella multocida

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(441)

&lt;220&gt;

&lt;223&gt; unknown C3

&lt;400&gt; 55

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atg ata aaa tat tta gag gga aat att aac tcg ttt ata tcg gca tta 48
Met Ile Lys Tyr Leu Glu Gly Asn Ile Asn Ser Phe Ile Ser Ala Leu
  1           5           10           15

ggt aaa aac gaa agt aat aaa gat att tta aaa tta gta gaa ata gtt 96
Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val
          20           25           30

tct tca gat ttt gaa gtg gat gaa cta agt cat aaa gat gaa cac gag 144
Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu
          35           40           45

ata tat tat ttg ttt tat aag agg ggt gtt gaa ttt tgt ttt aaa aga 192
Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg
          50           55           60

ata gat gaa gag tat gtc tta tat tcg gtt ttc ttt ttc ttg gta gag 240
Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Phe Leu Val Glu
          65           70           75           80

ggt gat aat tat ttt tca tgc cca ttt att cat gaa tta ata tgt gat 288
Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp
          85           90           95

ctt aaa cac gga ttc tca ata gag gat att ata agg ttt tta ggg gag 336
Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu
          100          105          110

cca aat ttt aaa ggt agt ggc tgg gta aga tat tct tat aat gga aga 384
Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg
          115          120          125

aat att cat ttc gaa ttt aat gaa tct aat gaa tta tcc cag att agc 432
Asn Ile His Phe Glu Phe Asn Glu Ser Asn Glu Leu Ser Gln Ile Ser
          130          135          140

att ttt att ta
Ile Phe Ile
145

```

&lt;210&gt; 56

&lt;211&gt; 147

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 56

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Met Ile Lys Tyr Leu Glu Gly Asn Ile Asn Ser Phe Ile Ser Ala Leu
  1           5           10           15

Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val
          20           25           30

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Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu  
           35                          40                          45  
 Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg  
           50                          55                          60  
 Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Phe Leu Val Glu  
           65                          70                          75                          80  
 Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp  
                           85                          90                          95  
 Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu  
                           100                          105                          110  
 Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg  
                           115                          120                          125  
 Asn Ile His Phe Glu Phe Asn Glu Ser Asn Glu Leu Ser Gln Ile Ser  
           130                          135                          140  
 Ile Phe Ile  
 145

<210> 57  
 <211> 8498  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <223> unknown C

<400> 57  
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 caattatcaa ttgttgaaat ttatcctttc aatgaagaac aagggatagc ttttcataat 120  
 aaaagtgtgg tacaacttaa accagaagag gtggaatggt catcaatcca ttatcctttc 180  
 tttgctggcg atattcagca agtcgctcat ctgcgaaaag ccgcagaaat ggggtgcgtg 240  
 gtgattgata tgaaagggat ttgtgccagc ttgcaagacg tccctgtggt gataccggga 300  
 gtaaatcagg aaaaattggt agatttacgt cagcgtaata ttgtgtcctt agccgatcca 360  
 caagtgcac aacttgcatt agtcacgccc tcgttgatgt caaatcacga aatcaaagac 420  
 attgccgtaa cctcgttatt acctgcattt tataactaac gagaaacggt aggtaaatta 480  
 gcgggacaaa cagcgcgatt gttaaattggc attccacttg atgaaggcga acaacgttta 540  
 gcttttgatg ttttccttac gcctgcacgc catttaaata tgcaaattca caagatcttt 600  
 ccacaattag ataatgtcgt atttcattct atccaagtgc ctgtttttcta cgggatgggg 660  
 caaatggtga gcgtattatc ggattatgca ttagatcctc aatcttgctt agcgagctgg 720  
 actgacaatc cgttgatgac ttatcatgca gaaaaatatt gcacccagc gacgaatggc 780  
 gaacaggaaa tggcagaaga gcaagcagca aaattacata taagtgggtt aagtgcggtg 840  
 gaaaatggtc tacaattttg gtcggttgca gatgaacagc gctttaatct tgctttattg 900

agtggtacgc ttgcagagtt aattttactcg caagggttatt aattttaaagtg tgtttttgca 960  
 cgatattttt atcttgaact ttgagagcgc actcgttttt gacgagtgcg tttttgttaa 1020  
 aacattcggtt tgaaagacag tgaatgaata gcggagttat tgataagaat caattttatac 1080  
 aaaagcaact gaatgttatt aatcgaggca ataaacctat tgatagtttt agttggcgcc 1140  
 ataatacata aactgtactt aataatatgc aatcaatacc tagaaatatt catgacgtaa 1200  
 tccaacatat cggggagggg attttaagtg atggtagaaa aaacatttag aaatctaaaa 1260  
 atatatgatg attatgggtc tgtctctcag gaaattattt ttaattttga aaaagagttt 1320  
 gatataaaac tccctttatc ctatatctca cttgtgaaaa agtataatgg cgtttggttt 1380  
 aaggaaagtg attttgaata tttatctcaa aatgggaaaa gaataataag ctcatgtagt 1440  
 tttgatagtt ttgagacaaa agataatatc gaaccaatga ataatatatt aagacaatat 1500  
 atttatgatg atgaaattta tggatataag aatgtttatt cctttgggta cactggaaat 1560  
 ggtgactttg tctgttttga ttatcgtgat gacccaaaag gtgatgagcc caaaatctgt 1620  
 atcgtgatc atgatgaata tgatgaaaaa acaggcaagc gtttgttatt gcctgtggca 1680  
 gaaaattttg aggcattttt agatatgctt tacgattttg atgaacgcta tccgaatggg 1740  
 tatgaatagg tatttgttta aataatgtgt tgtatttttt aagcattatt tacaactaac 1800  
 attttaagtg cgggtcaattt tgaaaaagt ttgggctttg agaattgggc gcattttttt 1860  
 tgaaatatc ttcaatgatg agcactaatt atggattaga taatgggaat tatcgagata 1920  
 tggatggtaa taaaggatgg aggctagatt ttgatcctga gaaagttgtt catgtaaata 1980  
 tttttgactt tactaaagg taaaggactag gtaaagcagt taaaaagtca ttctttttga 2040  
 tagtactgaa caagagtttg aaaaatttta aagcaattaa ataaggaaga taaaatgaca 2100  
 ttatttgatg aatgtaaatt agctcttaga gacgatttta atctaatttg tgatgaagag 2160  
 aaggattgtg taatggataa gttttatttc tatttcttgg aaaagaaaga ggaatttaat 2220  
 tttcaagatt attcatttga agaaatgtat atattttcaa aaatggaacc tgtgtatgtt 2280  
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Cys Val Gly Asp Gln Tyr Tyr Thr Ala Tyr Ser Lys Glu Glu Leu Leu	
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Asp Ser Phe Lys Gln Ile Ile Gly Phe Glu Glu Val Gly Arg Ser	
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Ser Ser His Lys Pro Lys Phe	
585	

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&lt;210&gt; 59

&lt;211&gt; 587

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 59

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Val Val Leu Asp Lys Ala Arg Leu Ala Gln Gly Met Asp Gln Ala Ala

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Tyr	Asp	Lys	Phe	His	Ser	Ser	Thr	Cys	Arg	Gly	Ser	Gly	Ser	Ser	Arg
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Thr	Cys	Gln	Ile	Asp	Ala	Asn	Pro	Lys	Lys	Ile	Met	Asp	Tyr	Ala	Leu
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Lys	Ile	Asn	Asp	Trp	Thr	Thr	Ile	Arg	Glu	Leu	Phe	Asn	Thr	Tyr	Ile
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 ttattattat caggcctata ttatttatat gcagtaaaaa acgattcaaa ttttgtcata 180  
 ggtttatcta ttatttttagt ttttattatt gtcattccag ggattttgac aaatgctatt 240  
 ttgaaagcta aggtgaaaaa aatcatggta gatttaccag gttttattga cttagttgca 300  
 gtaaatgttc aaacagggat tagtattgat gcggctttaa aacaagtggc aatcgatttt 360

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ttaattctag caccaggtat aatgagggtta tttccaa atg ttt ttt aaa ttt acc 715
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aag aaa atc gtt ttt gtt agt tta gct tta tct gtc gtt ggt tgt tct 763
Lys Lys Ile Val Phe Val Ser Leu Ala Leu Ser Val Val Gly Cys Ser
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acc cat tct cag caa ggc atg aca cag aaa agt atg tca tct gaa aca 811
Thr His Ser Gln Gln Gly Met Thr Gln Lys Ser Met Ser Ser Glu Thr
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ata acg gca aaa gag act tta tat gaa agt acg caa aat tat tcg gca 859
Ile Thr Ala Lys Glu Thr Leu Tyr Glu Ser Thr Gln Asn Tyr Ser Ala
                               40           45           50

ctc att tca ctg tat cgc gat gtg ttg aaa gcc aaa gaa gat cct tca 907
Leu Ile Ser Leu Tyr Arg Asp Val Leu Lys Ala Lys Glu Asp Pro Ser
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ata cgc tat aaa tta gcg aag aca tac tat cag cga ggt gac agc aaa 955
Ile Arg Tyr Lys Leu Ala Lys Thr Tyr Tyr Gln Arg Gly Asp Ser Lys
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tct tct tta ctt tat tta acg cca tta ctg aat gat aat acg aag ctt 1003
Ser Ser Leu Leu Tyr Leu Thr Pro Leu Leu Asn Asp Asn Thr Lys Leu
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gct aca caa gcg aaa ata tta cag ata aaa aat cta att caa tta aat 1051
Ala Thr Gln Ala Lys Ile Leu Gln Ile Lys Asn Leu Ile Gln Leu Asn
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aat ttc caa gaa gca att tct gtc gca aat gaa ctc tta tta aaa tca 1099
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aat ggg aat ttg gtg aat gcc cga aat gat atc aat aaa gca aga gag 1195
Asn Gly Asn Leu Val Asn Ala Arg Asn Asp Ile Asn Lys Ala Arg Glu
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att att aat ggc gat ttt aat aat gct gtt tct tta ctg ttg cca caa 1291
Ile Ile Asn Gly Asp Phe Asn Asn Ala Val Ser Leu Leu Leu Pro Gln
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tat tta aat ggc gtt aag aat tct cga ttg att cat aat ctt gtt ttt 1339

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 Ala Leu Val Lys Asn Gly Asp Leu Asp Tyr Ala Lys Asp Ile Ile Val  
 215 220 225 230  
 aaa gag cgt tta aat act tca cca gat gat tta att aat gca ttg aaa 1435  
 Lys Glu Arg Leu Asn Thr Ser Pro Asp Asp Leu Ile Asn Ala Leu Lys  
 235 240 245  
 aaa act aca cat gta tca aaa ggt gta act cgg taacactaag gatttgatat 1488  
 Lys Thr Thr His Val Ser Lys Gly Val Thr Arg  
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&lt;210&gt; 61

&lt;211&gt; 257

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 61

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Arg

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 Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala  
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 Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala  
 35 40 45  
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 Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly  
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 65 70 75 80  
 acc gaa caa ggc agc att tat aac ata ggc ggt atc ttg ggg gcg ggt 288  
 Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly

85	90	95	
aaa agt ttg aat ctg agc gcg aaa	aga gga gaa aac caa gga gga tat	336	
Lys Ser Leu Asn Leu Ser Ala Lys	Arg Gly Glu Asn Gln Gly Gly Tyr		
100	105	110	
ctt att aat caa ggt aag agt cta ctc cat tct gaa ggc gcc atg aac	384		
Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn			
115	120	125	
ctc aca gcg gat cgc acg gty tac aat tta ggg aat att ttt gct aaa	432		
Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys			
130	135	140	
ggg gac gcg acg atc aat gca aac gcg tta att aat gat gtt act ctc	480		
Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu			
145	150	155	160
aca ggt cgt ctt gag tat caa gat ctg aaa aaa gat tat acg cgt tat	528		
Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr			
165	170	175	
tat cgt atc aat gaa acg gca aaa cat ggt tgg cat aat aac ttc tat	576		
Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr			
180	185	190	
gaa tta aac gtc gac aga gtt tct tgatttgtgc atcaattttg taaccaccgg	630		
Glu Leu Asn Val Asp Arg Val Ser			
195	200		
ttaataaaac accagcaatt tcaacgccat tcatggcaga taatgccgct ggcacgatca	690		
catcaggacg atccgcggaa gtgacaagta aacttccaac gcggaaatgt tccaccatat	750		
tggtcaaatt acgtgcacag aaagtgatgc cacgaatgcg acgttcattg atcgcgctt	810		
catgaataat ggcagcacct aaatgtttgg ctaaataaat ggcacgagtc gcaattaatt	870		
ctgcgctcca aggaatacat gccaaagattt taattgggct tttctcaaat aaatgataaa	930		
tctcagatac ttgattttgt gtgtgttgga aagaatcaaa aatttctgcc aagtcagggc	990		
gagtacgacc agattcatca atcggcgcgt taaatttatt gatcacaaca ccaagtaaat	1050		
tagggttatt tttgctgcca aataatgagg ctgcggcttt gatgcgttct ttgagttctg	1110		
cgggtgtttc cgtcgccggt gctgcaacaa gaatgatttc cgcatcaagt gcttgagcaa	1170		
tttcatagtt aatgctattg gcataagaat gcttacgcgt agggattaaa ccttcacca	1230		
cgacaatttc atgttttttg gcgagttggt gatgattttc aacaattttt tctagtacca	1290		
catcagattg attttgaccg atgagtgatt cagctacact taacataaat ggttcactgg	1350		
tttcaatggt ggtactggtg cgaataattg atgttgtgcg atcaatcata tcttcacctg	1410		
agttcggctg agaaattggt ttcataaagc cgactttcgc ccctttttgc tccagtgc	1470		
gtgttaaacc taagctgaca ctgggtaagc ctacaccagc actaatcggg ataaggataa	1530		
ttgtacgtga cataataaac cctaatttgt tgataattta tacaaaaaga aactgccgat	1590		
gaatcggcag ttaattgatc tttacgcgat gcaaaggcgc gcggtatctt gtgcaataac	1650		

aagttcttca ttcgttggga tcaccatggc aacaggcgta ttgtctgctg taatcaccce 1710  
 ttcatgacca aagcgagccg ctttgttttt atctgaatcc acttgataac cgaacagttt 1770  
 taaatgggtt aaggttga 1788

<210> 63  
 <211> 200  
 <212> PRT  
 <213> Pasteurella multocida

<400> 63  
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 Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala  
             20                    25                    30  
 Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala  
             35                    40                    45  
 Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly  
             50                    55                    60  
 Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn  
     65                    70                    75                    80  
 Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly  
             85                    90                    95  
 Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr  
             100                    105                    110  
 Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn  
             115                    120                    125  
 Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys  
     130                    135                    140  
 Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu  
     145                    150                    155                    160  
 Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr  
             165                    170                    175  
 Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr  
             180                    185                    190  
 Glu Leu Asn Val Asp Arg Val Ser  
     195                    200

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 <212> DNA  
 <213> Pasteurella multocida

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<223> unknown O

<400> 64

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cattacccaa atggaaataa accttaacca tagcaagaga gaagaaa atg aaa att 116
                                     Met Lys Ile
                                     1

act att aca cga aat cat cca gaa gta ttt caa gaa tcc gct cgt tta 164
Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser Ala Arg Leu
      5              10              15

gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca tta aca ttg 212
Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala Leu Thr Leu
      20              25              30              35

gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt gag gag gaa 260
Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly Glu Glu Glu
      40              45              50

agc aaa agg gga cat agt 278
Ser Lys Arg Gly His Ser
      55

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<210> 65

<211> 57

<212> PRT

<213> *Pasteurella multocida*

<400> 65

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Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
  1              5              10              15

Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
      20              25              30

Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
      35              40              45

Glu Glu Glu Ser Lys Arg Gly His Ser
      50              55

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<210> 66

<211> 1020

<212> DNA

<213> *Pasteurella multocida*

<220>

<221> CDS

<222> (1)..(597)

<220>

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<400> 66

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Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala
  1              5              10              15

gca atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att 96

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Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile
      20              25              30

tca aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat 144
Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr
      35              40              45

ttt gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa 192
Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
      50              55              60

ggc atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta 240
Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu
      65              70              75              80

cgc acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc 288
Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg
      85              90              95

act gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca 336
Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala
      100              105              110

gtg gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca 384
Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala
      115              120              125

atc aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc 432
Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly
      130              135              140

ggg aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa 480
Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys
      145              150              155              160

gat gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc 528
Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu
      165              170              175

gaa cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat 576
Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp
      180              185              190

ttt tca aat cgt tta gca tcg taaggggtag aaaatggcctt taccacgcaa 627
Phe Ser Asn Arg Leu Ala Ser
      195

acttaaattg atgaatttaa tcatcgacgg taacaaatat ctcggcgaag tcacggaagt 687

gactcaacca aaattagcaa tgaaaatcga agaatttcgc gcgggcggta tgattggttc 747

gggtgatgtc aatctcgggc ttgaaaagct cgaagcggaa tttaaagccg gtggctacat 807

ggtcgaatta attaaaaaat tcggcgggtc aatcaacggc attccattgc gttttcttgg 867

ctcatatcag cgtgatgaca cagaagaagt cacatctgtt gagcttgtga tgcaaggtcg 927

atttactgaa attgacagcg gaaacagcaa agtgggcat gacactgaac aaacattcaa 987

agtgcccttta acgtattaca aaatcattgt tga 1020

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&lt;210&gt; 67



&lt;211&gt; 199

&lt;212&gt; PRT

<213> *Pasteurella multocida*

&lt;400&gt; 67

Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala  
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Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile  
 20 25 30

Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr  
 35 40 45

Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln  
 50 55 60

Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu  
 65 70 75 80

Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg  
 85 90 95

Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala  
 100 105 110

Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala  
 115 120 125

Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly  
 130 135 140

Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys  
 145 150 155 160

Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu  
 165 170 175

Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp  
 180 185 190

Phe Ser Asn Arg Leu Ala Ser  
 195

&lt;210&gt; 68

&lt;211&gt; 2584

&lt;212&gt; DNA

<213> *Pasteurella multocida*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1042)..(2286)

&lt;220&gt;

&lt;223&gt; xylA

&lt;400&gt; 68

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taccattatt ttatggaatc tctctggacc gatgaccatt gccaatattg aaattcctca 120

cgcgatggtc tttttggctt ttatttacgt gctgttttagc agtattgtgg catttaaaat 180

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cggtcgcccg ttaattcagc tcaattttgc caatgaacgc ttaaacgcca actaccgtta 240
ttcacttatc cgtctgaaag aatatgctga aagcattgct ttttatcgtg gtgaaaaaat 300
ggaaaaacgt ctattgacca cacaatttaa tcagggtgatt gataacgttt ggcaagtaat 360
ctaccgcacc ttgaaattat ccggttttaa cttaatcatt acgcagattt cggtgggtttt 420
tccgctgggtg attcaagtga cacgttattt tcgtcgacaa taggtgcata tgaggggtgtt 480
agaatagcga tacttttctgt tggaaaagta aactctttaa tataaataga aatcgcttga 540
atgattctcg ggcaaaaaat aatgtactca tttgcatct catactgata atggcgaagt 600
aaatatcttc ttacaatatt atggtaatta tcaggtaata ccgtatagcc atagattcca 660
gttctatttt gttttgctaa ataattgatg agcatttgag gcgcaggtaa atccatatct 720
gcaacagaca ttgaaatcat atccttgccg tatttacgag taattgccca tttagcacta 780
tgacaatctg atctatcagt aaaaacatca aacaaattat ccgtcataca tgttctccaa 840
tattggattt atataaactt tagaacttga ggtagattgt tggaattgtt aaatctggta 900
tttctattac gttttttctt ttttgtgata taagccacaa taaccaataa tcttaattgt 960
taagtgaat aacgtaattg atcctcccat tgttttacta aattatgtct ctgaaactta 1020
tttgttcagg agaaatcatt t atg tcc act tac ttc gac aaa att gaa aaa 1071
                        Met Ser Thr Tyr Phe Asp Lys Ile Glu Lys
                        1                      5                      10

gta aat tat gaa ggt gta act tca tct aat ccg ttt gca tat aag cat 1119
Val Asn Tyr Glu Gly Val Thr Ser Ser Asn Pro Phe Ala Tyr Lys His
                        15                      20                      25

tat gat gct aat caa gtt att tta ggt aag acg atg gct gaa cac tta 1167
Tyr Asp Ala Asn Gln Val Ile Leu Gly Lys Thr Met Ala Glu His Leu
                        30                      35                      40

cgt tta gcc gtc tgt tat tgg cac act ttc tgt tgg aca ggg aat gat 1215
Arg Leu Ala Val Cys Tyr Trp His Thr Phe Cys Trp Thr Gly Asn Asp
                        45                      50                      55

atg ttc ggt gtc ggt tct ttc gat cgt tgt tgg cag aag gcg agt gat 1263
Met Phe Gly Val Gly Ser Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp
                        60                      65                      70

tca tta gca ggt gca aaa caa aaa gca gat atc gct ttt gaa ttt ttc 1311
Ser Leu Ala Gly Ala Lys Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe
                        75                      80                      85                      90

agt aaa tta ggc ata cct tat tat tgt ttt cat gat gtt gat gtt gcg 1359
Ser Lys Leu Gly Ile Pro Tyr Tyr Cys Phe His Asp Val Asp Val Ala
                        95                      100                      105

cca gaa ggt cat tca ttt aaa gaa tat ttg tcg aac ttt aat aca atg 1407
Pro Glu Gly His Ser Phe Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met
                        110                      115                      120

atc gat gtt tta gcg cag aaa caa gaa gaa aca ggc gtc aaa ttg ttg 1455
Ile Asp Val Leu Ala Gln Lys Gln Glu Glu Thr Gly Val Lys Leu Leu
                        125                      130                      135

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tgg Trp	ggg Gly 140	act Thr	gca Ala	aat Asn	tgt Cys 145	ttt Phe	aca Thr	cac His	cct Pro	cgt Arg	tat Tyr 150	atg Met	tct Ser	ggg Gly	gct Ala	1503
gca Ala 155	aca Thr	aat Asn	ccg Pro	aat Asn 160	cca Pro	gaa Glu	att Ile	ttt Phe	gct Ala 165	tgg Trp	gct Ala	gct Ala	gca Ala	caa Gln	gta Val 170	1551
ttt Phe	act Thr	gcc Ala	atg Met	ggg Gly 175	gca Ala	act Thr	cag Gln	cgt Arg	tta Leu 180	ggg Gly	ggg Gly	gaa Glu	aat Asn	tat Tyr 185	gtt Val	1599
ttg Leu	tgg Trp	gga Gly	gga Gly 190	cgt Arg	gaa Glu	gga Gly	tat Tyr	gaa Glu 195	acg Thr	tta Leu	tta Leu	aat Asn 200	acc Thr	aat Asn	tta Leu	1647
aaa Lys	cag Gln 205	gag Glu	cga Arg	gag Glu	caa Gln	att Ile	gga Gly 210	cgt Arg	ttc Phe	atg Met	caa Gln 215	atg Met	gtg Val	gtt Val	gag Glu	1695
cat His 220	aaa Lys	tat Tyr	aaa Lys	atc Ile	ggg Gly	ttt Phe 225	aac Asn	ggg Gly	act Thr	ttg Leu	ctg Leu 230	att Ile	gaa Glu	cca Pro	aag Lys	1743
cca Pro 235	caa Gln	gag Glu	cca Pro	acg Thr 240	aaa Lys	cat His	caa Gln	tat Tyr	gac Asp 245	tat Tyr	gat Asp	gtg Val	gcg Ala	acc Thr	gtt Val 250	1791
tat Tyr	ggc Gly	ttt Phe	tta Leu	aag Lys 255	cag Gln	ttt Phe	ggg Gly	tta Leu	gaa Glu 260	aaa Lys	gaa Glu	att Ile	aaa Lys 265	gtg Val	aat Asn	1839
att Ile	gaa Glu	gct Ala	aat Asn 270	cac His	gca Ala	aca Thr	tta Leu	gct Ala 275	gga Gly	cac His	act Thr	ttc Phe 280	cag Gln	cat His	gaa Glu	1887
gtc Val	gcc Ala 285	atg Met	gct Ala	aca Thr	gcg Ala	tta Leu	gat Asp 290	att Ile	ttt Phe	ggg Gly	tct Ser	att Ile 295	gat Asp	gca Ala	aat Asn	1935
cgt Arg	ggg Gly 300	gat Asp	cca Pro	caa Gln	tta Leu	ggg Gly 305	tgg Trp	gat Asp	acc Thr	gat Asp	caa Gln 310	ttc Phe	cct Pro	aat Asn	agc Ser	1983
gta Val 315	gaa Glu	gaa Glu	aat Asn	act Thr 320	ttg Leu	gtc Val	ata Ile	tat Tyr	gaa Glu 325	att Ile	ctc Leu	aaa Lys	gca Ala	ggg Gly 330	ggc Gly 330	2031
ttt Phe	aca Thr	acc Thr	ggg Gly 335	ggg Gly	ttt Phe	aat Asn	ttt Phe	gat Asp 340	gct Ala	aaa Lys	atc Ile	cgt Arg	cgg Arg	cag Gln 345	agt Ser	2079
acg Thr	gat Asp	cct Pro	tac Tyr 350	gat Asp	tta Leu	ttt Phe	cat His	gga Gly 355	cat His	att Ile	ggc Gly	gcg Ala	att Ile 360	gat Asp	gta Val	2127
ctt Leu	gcc Ala 365	tta Leu	tca Ser	cta Leu	aaa Lys	tgt Cys	gcg Ala	gcg Ala 370	aaa Lys	atg Met	ctt Leu	gaa Glu 375	gag Glu	caa Gln	gct Ala	2175
tta Leu	caa Gln 380	aaa Lys	gtc Val	gtc Val	aat Asn	caa Gln 385	cgt Arg	tat Tyr	gct Ala	ggg Gly 390	tgg Trp	aca Thr	tca Ser	tca Ser	ctt Leu	2223

ggt caa ctt gtt caa atc cgg tcc tac cac gcg tgt ctg caa tac aga 2271  
 Gly Gln Leu Val Gln Ile Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg  
 395 400 405 410

cta aca aaa gtg ctt taaaacgttc cggcttacgc cagacatcta gacgattgaa 2326  
 Leu Thr Lys Val Leu  
 415

taatttcaat attgtctccg cacgtaattc aaaggctttg tgtatgtgcg aatgatattc 2386

acaacaaagt tctgcaaaat cttgaattgc gtgaggtaat ttaaagcgct gacataagcg 2446

tcttgctggc atgacaccag ctttttcatg tccataatga tgtggcaata tttcttttgg 2506

tgtaaggct tttcctaaat catgacaaat tgcagcaaaa cgtaccgcac ttttgtcact 2566

gtccgtgttt tctgtcga 2584

<210> 69

<211> 415

<212> PRT

<213> Pasteurella multocida

<400> 69

Met Ser Thr Tyr Phe Asp Lys Ile Glu Lys Val Asn Tyr Glu Gly Val  
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Thr Ser Ser Asn Pro Phe Ala Tyr Lys His Tyr Asp Ala Asn Gln Val  
 20 25 30

Ile Leu Gly Lys Thr Met Ala Glu His Leu Arg Leu Ala Val Cys Tyr  
 35 40 45

Trp His Thr Phe Cys Trp Thr Gly Asn Asp Met Phe Gly Val Gly Ser  
 50 55 60

Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp Ser Leu Ala Gly Ala Lys  
 65 70 75 80

Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe Ser Lys Leu Gly Ile Pro  
 85 90 95

Tyr Tyr Cys Phe His Asp Val Asp Val Ala Pro Glu Gly His Ser Phe  
 100 105 110

Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met Ile Asp Val Leu Ala Gln  
 115 120 125

Lys Gln Glu Glu Thr Gly Val Lys Leu Leu Trp Gly Thr Ala Asn Cys  
 130 135 140

Phe Thr His Pro Arg Tyr Met Ser Gly Ala Ala Thr Asn Pro Asn Pro  
 145 150 155 160

Glu Ile Phe Ala Trp Ala Ala Ala Gln Val Phe Thr Ala Met Gly Ala  
 165 170 175

Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val Leu Trp Gly Gly Arg Glu  
 180 185 190

Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu Lys Gln Glu Arg Glu Gln  
 195 200 205

Ile Gly Arg Phe Met Gln Met Val Val Glu His Lys Tyr Lys Ile Gly  
 210 215 220  
 Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys Pro Gln Glu Pro Thr Lys  
 225 230 235 240  
 His Gln Tyr Asp Tyr Asp Val Ala Thr Val Tyr Gly Phe Leu Lys Gln  
 245 250 255  
 Phe Gly Leu Glu Lys Glu Ile Lys Val Asn Ile Glu Ala Asn His Ala  
 260 265 270  
 Thr Leu Ala Gly His Thr Phe Gln His Glu Val Ala Met Ala Thr Ala  
 275 280 285  
 Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn Arg Gly Asp Pro Gln Leu  
 290 295 300  
 Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser Val Glu Glu Asn Thr Leu  
 305 310 315 320  
 Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly Phe Thr Thr Gly Gly Phe  
 325 330 335  
 Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser Thr Asp Pro Tyr Asp Leu  
 340 345 350  
 Phe His Gly His Ile Gly Ala Ile Asp Val Leu Ala Leu Ser Leu Lys  
 355 360 365  
 Cys Ala Ala Lys Met Leu Glu Glu Gln Ala Leu Gln Lys Val Val Asn  
 370 375 380  
 Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu Gly Gln Leu Val Gln Ile  
 385 390 395 400  
 Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg Leu Thr Lys Val Leu  
 405 410 415

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 <222> (298)..(1905)

<220>  
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 gtcaagaata atgtgatgtt accggtgatt aataccaata ttgaaccgca ctttgatgcc 180  
 cttagagcca cccaaatgaa cacgaaagt ctcgatacct caaaagtgaa tgccgaacaa 240  
 gtcaaaaaat ggattgctgt ttggcaaagc accctaacc aataattgtt tgtcttg 297

atg ttt aag cga ttt cgt gca ttc aca tac cgt ccc gcc agt tat ctt	345
Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu	
1 5 10 15	
ggc ggg atg ttg gtg att gtt ttt ctg agc gct ttt tat gcg ttc gcc	393
Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala	
20 25 30	
tta ggg gcg gtt ttt tcg ctc cct ttt gcg cgc agt tgg aca gcg ttg	441
Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu	
35 40 45	
ttg agt gat cag tat tta caa cac gtg atc atc ttt agc ttt tgg caa	489
Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln	
50 55 60	
gcc ttt ctg tcg gcg gta ctt gcg gtc ctc ttt ggt gcc att gta gca	537
Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala	
65 70 75 80	
cga gcc ttt ttt tat caa ccg ttt gtg ggc aag aaa ctg atc ctc aaa	585
Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys	
85 90 95	
tta ttt tca ctg act ttt gtg tta cct gcc tta gtg gcg att ttt ggt	633
Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly	
100 105 110	
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Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln	
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Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile	
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tta ctg gcg cat ctt ttt ttt aat gtc cca tta gct tgt cgc ctg ttt	777
Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe	
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tta caa ggt ttg caa gca att ccg gtg caa caa cgt cag ctc gcg gca	825
Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala	
165 170 175	
caa ctc aat tta cgt ggt tgg cat ttt ata cgt ctg att gag tgg ccc	873
Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro	
180 185 190	
tat tta cgc cag caa ttg tta cct gca ttt act ttg att ttc atg ctg	921
Tyr Leu Arg Gln Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu	
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Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Gly Pro Lys	
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tat acc acg ttg gaa gtg gct atc tat caa gcg att tta ttt gag ttt	1017
Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe	
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gat gta ccg aaa gcc ggc tta ttt gcg tta tta caa ttt gtt ttt tgt	1065
Asp Val Pro Lys Ala Gly Leu Phe Ala Leu Leu Leu Gln Phe Val Phe Cys	
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Phe Leu Leu Phe Thr Leu Ser Ser Phe Phe Ser Pro Ala Pro Ala Thr	
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Thr Leu His Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val	
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Lys Leu Trp Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu	
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Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe	
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Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser	
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Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Ala Leu Val Leu Ser Phe	
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Ala Leu Leu Leu Leu Ala Arg Gln Leu His Trp Arg His Tyr Arg Ser	
355 360 365	
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Leu Ser His Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro	
370 375 380	
acg tta gtg tta gct att ggt tta ttc att tta tta cgt gag atc gat	1497
Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp	
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Phe Ser Pro Tyr His Leu Phe Gly Val Val Val Cys Cys Asn Ala Leu	
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gct gct atg cct ttt gtg ttg cgt att ttg gct tta ccg atg cat aac	1593
Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn	
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Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly	
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Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met	
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Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr	
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Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu	
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Leu Tyr Gln Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr	
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Arg His Gln Glu Pro Arg Asp Asp
      530                      535

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attggatgaa cttttttctg ccttagatcc cgatttacgg gcagaaatgt tgcattttatt 2415

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cagaatttgt gcgcactatt gcggtggcgc gtattaccat gccgaaaagc tatgtacgtt 3435

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3501



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 <213> Pasteurella multocida

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Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu
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Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln
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Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala
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Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys
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Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly
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Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln
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Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe
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Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala
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Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro
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Tyr Leu Arg Gln Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu
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Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Gly Pro Lys
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Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe
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Asp Val Pro Lys Ala Gly Leu Phe Ala Leu Leu Gln Phe Val Phe Cys
      245          250          255

Phe Leu Leu Phe Thr Leu Ser Ser Phe Phe Ser Pro Ala Pro Ala Thr
      260          265          270

Thr Leu His Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val
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Lys Leu Trp Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu
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 485 490 495  
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Leu Gly Phe Leu Thr Gly Leu Ile Ala Leu Val Ile Ser Tyr Leu Trp	
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Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser Arg Val Thr Asp	
70 75 80	
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Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met Phe Val Leu Met	
85 90 95 100	
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Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp Leu Tyr Asn Ala	
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Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser Ser Glu Asn His	
230 235 240	
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Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile Ile His Asp Ile Ala Ile	
245 250 255 260	
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Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile Tyr Gly Gly Ile	
265 270 275	
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280 285 290	

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 Ser Tyr Leu Trp Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser  
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 Phe Val Leu Met Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp  
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 115 120 125  
 Ala Ile Gln Ser Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly  
 130 135 140  
 Ile Ile Gly Gly Glu Thr Val Leu Leu Gly Met Leu Ala Leu Pro Gln  
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 Met Leu Arg Leu Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val  
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 Ala Gly Gly Ala Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile  
 180 185 190  
 Ile Tyr Gly Met Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala  
 195 200 205  
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 Leu Val Leu Cys Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser  
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 245 250 255  
 Asp Ile Ala Ile Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile  
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 Tyr Gly Gly Ile Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val  
 275 280 285  
 Gly Val Ile Leu Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile  
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 Val Gln Glu Ser Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile  
 305 310 315 320  
 Trp Val Gly Ile Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met  
 325 330 335  
 Gly Gly Asp Arg Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser  
 340 345 350  
 Pro Ile Tyr Thr Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly  
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 Met Phe Leu Asp Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr  
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Ser Lys Ala Thr ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile  
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Val Gly Arg Gly Thr Phe  
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 Met Val Leu Pro  
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ata att tct acc cct aag ttg tgg caa tac atc cct tct tca aaa tta 522  
 Ile Ile Ser Thr Pro Lys Leu Trp Gln Tyr Ile Pro Ser Ser Lys Leu  
 5 10 15 20

gaa caa tcc gcc atg gct aaa caa cct aat tct ttg att cgt tta ata 570  
 Glu Gln Ser Ala Met Ala Lys Gln Pro Asn Ser Leu Ile Arg Leu Ile  
 25 30 35

atg gct tca cgt gta gtt gga cgg acg cga tcg gta cca tca aaa gca 618  
 Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val Pro Ser Lys Ala  
 40 45 50

ata ata tcg gcg cct gct gcg gct aac tct tca atg tct tgt aaa aat 666  
 Ile Ile Ser Ala Pro Ala Ala Ala Asn Ser Ser Met Ser Cys Lys Asn  
 55 60 65

ggg cta ata cga acg gga ctg tca ggt aaa tcg cgt tta acg ata cca 714  
 Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg Leu Thr Ile Pro  
 70 75 80

ata atc ggt aca ttg acg acg tta cgc gtg gct ttt aaa ttt tcg atc 762  
 Ile Ile Gly Thr Leu Thr Thr Leu Arg Val Ala Phe Lys Phe Ser Ile

| 85   | 90  | 95  | 100 |      |
|--|-----|-----|-----|------|
| cct tca ata cgt aac ccg gca gca cca ccg ata acg gat gct tgc gcc    |     |     |     | 810  |
| Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro Ile Thr Asp Ala Cys Ala    |     |     |     |      |
|  | 105 | 110 | 115 |      |
| atg gcg gca aca att tct ggc gag tcc att ggc cca tta tct acg ggc    |     |     |     | 858  |
| Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro Leu Ser Thr Gly    |     |     |     |      |
|  | 120 | 125 | 130 |      |
| tgg caa gat gcg att aag cca tat tta att tgt tct aaa act tgc gga    |     |     |     | 906  |
| Trp Gln Asp Ala Ile Lys Pro Tyr Leu Ile Cys Ser Lys Thr Cys Gly    |     |     |     |      |
|  | 135 | 140 | 145 |      |
| tgt gat agt ttt gac ata tta act cca gtc taaatttattc aaaagaagat     |     |     |     | 956  |
| Cys Asp Ser Phe Asp Ile Leu Thr Pro Val                            |     |     |     |      |
|  | 150 | 155 |     |      |
| tgactccaat ttgcataggt taatcttaga attaaaaaat aacaaccaa ataataaaaa   |     |     |     | 1016 |
| tttgagatct ttgtcgcata tttattcata gggaatagac agcttaattt tagttatgat  |     |     |     | 1076 |
| ttgtcaatcc ttgtattttt ttgtgtttgc tgggttgcg tacactgttc taatattgct   |     |     |     | 1136 |
| ttgagcactt gataaccttg ctcattaaaa tgtaatccgt cggtaaaaag gcgtaaatcc  |     |     |     | 1196 |
| agttcaccgt tagaatcaca aaagtatttt ttgtgtttcaa cgtaagtcac gtctgacgga |     |     |     | 1256 |
| caatgttggt ttaaataggt attgagcctg tgaatttggt cgtagtgac cgtattaatc   |     |     |     | 1316 |
| tgattgaccg gtgtggcttc taataaaaag tagtgggacg taggagaaat ggtgtgtagg  |     |     |     | 1376 |
| tgagtcagaa tgtcatttaa ctatcgcatg acttgccgcg gtgaatacgt ttcttcctta  |     |     |     | 1436 |
| caaatatcat tgacgcctaa aaaaagaaaa acagattgtc caagttggtg aatccgttta  |     |     |     | 1496 |
| ggtttaacga taacatccaa atattgtgc gtactgacgc cagaaagtcc taaattggcg   |     |     |     | 1556 |
| acggtttgct ccgctaattg aggtgtgcct gctacctgtt cgtcccacat gtcaaaaagt  |     |     |     | 1616 |
| gaatgaccaa ttaagctgat attggcaggt ttggaaaatt ccgccatttt gctctgatag  |     |     |     | 1676 |
| cgttgataaa tatcctgatc acttagcatg tgtggacctc tattttgaaa taaaacgcta  |     |     |     | 1736 |
| agtattatat aaaacctgat atgccggtaa acagtaaaact tatcttccgt aggggtaaat |     |     |     | 1796 |
| attcaatttt gtgacgaacc tatcatttat gaaataaaac ttcattttct atataaaaaa  |     |     |     | 1856 |
| tagttttttc actttagaat gccaaacgtg tgaaatttat ttcacatca ttttaacgta   |     |     |     | 1916 |
| atcccaacgt aaccaataga ggagaactca taatgaaatt taaaaaacta ctacttgcac  |     |     |     | 1976 |
| ctttatgttt aggtgtttca gcttctgtat ttgcagcaga ttacgatctt aaattcggta  |     |     |     | 2036 |
| tgggtgctggg tccaagctca aacgaatata aagcagtaga attctttgcg aaagaagtga |     |     |     | 2096 |
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| accgtgtgat gattaaacaa ttaaaagacg gtgcattaga ctttacgtta ggtgaatcag  |     |     |     | 2216 |
| cacgtttcca aatttacttc ccagaagcag aagtatttgc gttgccttat atgattccta  |     |     |     | 2276 |
| attttgaaac ctctaaaaaa gcgttgctcg acacaaaatt tggtaagggt ttattgaaaa  |     |     |     | 2336 |



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<210> 75

<211> 158

<212> PRT

<213> *Pasteurella multocida*

<400> 75

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| Met | Val | Leu | Pro | Ile | Ile | Ser | Thr | Pro | Lys | Leu | Trp | Gln | Tyr | Ile | Pro | 1   | 5   | 10  | 15 |
| Ser | Ser | Lys | Leu | Glu | Gln | Ser | Ala | Met | Ala | Lys | Gln | Pro | Asn | Ser | Leu | 20  | 25  | 30  |    |
| Ile | Arg | Leu | Ile | Met | Ala | Ser | Arg | Val | Val | Gly | Arg | Thr | Arg | Ser | Val | 35  | 40  | 45  |    |
| Pro | Ser | Lys | Ala | Ile | Ile | Ser | Ala | Pro | Ala | Ala | Ala | Asn | Ser | Ser | Met | 50  | 55  | 60  |    |
| Ser | Cys | Lys | Asn | Gly | Leu | Ile | Arg | Thr | Gly | Leu | Ser | Gly | Lys | Ser | Arg | 65  | 70  | 75  | 80 |
| Leu | Thr | Ile | Pro | Ile | Ile | Gly | Thr | Leu | Thr | Thr | Leu | Arg | Val | Ala | Phe | 85  | 90  | 95  |    |
| Lys | Phe | Ser | Ile | Pro | Ser | Ile | Arg | Asn | Pro | Ala | Ala | Pro | Pro | Ile | Thr | 100 | 105 | 110 |    |
| Asp | Ala | Cys | Ala | Met | Ala | Ala | Thr | Ile | Ser | Gly | Glu | Ser | Ile | Gly | Pro | 115 | 120 | 125 |    |
| Leu | Ser | Thr | Gly | Trp | Gln | Asp | Ala | Ile | Lys | Pro | Tyr | Leu | Ile | Cys | Ser | 130 | 135 | 140 |    |
| Lys | Thr | Cys | Gly | Cys | Asp | Ser | Phe | Asp | Ile | Leu | Thr | Pro | Val | 145 | 150 | 155 |     |     |    |

<210> 76

<211> 2787

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<213> *Pasteurella multocida*

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<221> CDS

<222> (1949)..(2785)

&lt;220&gt;

&lt;223&gt; yiaO

&lt;400&gt; 76

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aattttgtga cgaacctatc atttatgaaa taaaacttca ttttctatat aaaaaatagt 1860
tttttcactt tagaatgcc aacgtgtgaa atttatttca tcatcatttt aacgtaatcc 1920
caacgtaacc aatagaggag aactcata atg aaa ttt aaa aaa cta cta ctt 1972
                               Met Lys Phe Lys Lys Leu Leu Leu
                               1                               5

gca tct tta tgt tta ggt gtt tca gct tct gta ttt gca gca gat tac 2020
Ala Ser Leu Cys Leu Gly Val Ser Ala Ser Val Phe Ala Ala Asp Tyr
    10                               15                               20

gat ctt aaa ttc ggt atg gtt gcg ggt cca agc tca aac gaa tat aaa 2068
Asp Leu Lys Phe Gly Met Val Ala Gly Pro Ser Ser Asn Glu Tyr Lys
    25                               30                               35                               40

gca gta gaa ttc ttt gcg aaa gaa gtg aaa gaa aaa tcc aat ggc aaa 2116
Ala Val Glu Phe Phe Ala Lys Glu Val Lys Glu Lys Ser Asn Gly Lys
                               45                               50                               55

att gat gtg gct att ttc cct agc tca cag tta ggt gat gac cgt gtg 2164
Ile Asp Val Ala Ile Phe Pro Ser Ser Gln Leu Gly Asp Asp Arg Val
                               60                               65                               70

atg att aaa caa tta aaa gac ggt gca tta gac ttt acg tta ggt gaa 2212
Met Ile Lys Gln Leu Lys Asp Gly Ala Leu Asp Phe Thr Leu Gly Glu
    75                               80                               85

tca gca cgt ttc caa att tac ttc cca gaa gca gaa gta ttt gcg ttg 2260
Ser Ala Arg Phe Gln Ile Tyr Phe Pro Glu Ala Glu Val Phe Ala Leu
    90                               95                               100

cct tat atg att cct aat ttt gaa acc tct aaa aaa gcg ttg ctc gac 2308
Pro Tyr Met Ile Pro Asn Phe Glu Thr Ser Lys Lys Ala Leu Leu Asp
   105                               110                               115                               120

aca aaa ttt ggt caa ggt tta ttg aaa aaa att gat aaa gag tta aac 2356
Thr Lys Phe Gly Gln Gly Leu Leu Lys Lys Ile Asp Lys Glu Leu Asn
    125                               130                               135

gta caa gtg tta tct gtg gcg tat aac ggt aca cgt caa aca act tct 2404
Val Gln Val Leu Ser Val Ala Tyr Asn Gly Thr Arg Gln Thr Thr Ser
    140                               145                               150

aac cgt gca atc aac agc att gaa gac atg aaa ggg tta aaa tta cgt 2452
Asn Arg Ala Ile Asn Ser Ile Glu Asp Met Lys Gly Leu Lys Leu Arg
    155                               160                               165

gta cct aac gcg gca acc aac ctt gct tat gca aaa tac gtg ggt gca 2500
Val Pro Asn Ala Ala Thr Asn Leu Ala Tyr Ala Lys Tyr Val Gly Ala
    170                               175                               180

gcg cca aca cca atg gca ttc tct gaa gtt tac ctt gcg ctt caa aca 2548
Ala Pro Thr Pro Met Ala Phe Ser Glu Val Tyr Leu Ala Leu Gln Thr
   185                               190                               195                               200

aac tct gtg gat ggt caa gaa aac cca tta ccg aca atc caa gca caa 2596
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    205                               210                               215

aaa ttc tat gaa gta caa aaa tac tta gcg tta act aac cac atc tta 2644
Lys Phe Tyr Glu Val Gln Lys Tyr Leu Ala Leu Thr Asn His Ile Leu
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aat gac caa ctt tac tta atc agt aac gat acg ttg gca gat tta cca 2692  
Asn Asp Gln Leu Tyr Leu Ile Ser Asn Asp Thr Leu Ala Asp Leu Pro  
235 240 245

gaa gat tta caa aaa gtg gtt aaa gat gca gca gcg aaa gcc gct gaa 2740  
Glu Asp Leu Gln Lys Val Val Lys Asp Ala Ala Ala Lys Ala Ala Glu  
250 255 260

tat cac act aaa ctc ttc gtt gac ggt gag aac agc tta gtt gaa tt 2787  
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<210> 77

<211> 279

<212> PRT

<213> Pasteurella multocida

<400> 77

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Gly Pro Ser Ser Asn Glu Tyr Lys Ala Val Glu Phe Phe Ala Lys Glu  
35 40 45

Val Lys Glu Lys Ser Asn Gly Lys Ile Asp Val Ala Ile Phe Pro Ser  
50 55 60

Ser Gln Leu Gly Asp Asp Arg Val Met Ile Lys Gln Leu Lys Asp Gly  
65 70 75 80

Ala Leu Asp Phe Thr Leu Gly Glu Ser Ala Arg Phe Gln Ile Tyr Phe  
85 90 95

Pro Glu Ala Glu Val Phe Ala Leu Pro Tyr Met Ile Pro Asn Phe Glu  
100 105 110

Thr Ser Lys Lys Ala Leu Leu Asp Thr Lys Phe Gly Gln Gly Leu Leu  
115 120 125

Lys Lys Ile Asp Lys Glu Leu Asn Val Gln Val Leu Ser Val Ala Tyr  
130 135 140

Asn Gly Thr Arg Gln Thr Thr Ser Asn Arg Ala Ile Asn Ser Ile Glu  
145 150 155 160

Asp Met Lys Gly Leu Lys Leu Arg Val Pro Asn Ala Ala Thr Asn Leu  
165 170 175

Ala Tyr Ala Lys Tyr Val Gly Ala Ala Pro Thr Pro Met Ala Phe Ser  
180 185 190

Glu Val Tyr Leu Ala Leu Gln Thr Asn Ser Val Asp Gly Gln Glu Asn  
195 200 205

Pro Leu Pro Thr Ile Gln Ala Gln Lys Phe Tyr Glu Val Gln Lys Tyr  
210 215 220

Leu Ala Leu Thr Asn His Ile Leu Asn Asp Gln Leu Tyr Leu Ile Ser  
225 230 235 240

Asn Asp Thr Leu Ala Asp Leu Pro Glu Asp Leu Gln Lys Val Val Lys  
 245 250 255

Asp Ala Ala Ala Lys Ala Ala Glu Tyr His Thr Lys Leu Phe Val Asp  
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Gly Glu Asn Ser Leu Val Glu  
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<222> (908)..(1294)

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aaagtgcggg ggcaattcgt tttattgagc aagtggacga gaaattgatt ttccgcagcg 180

gtggcgggat tacgatctta agcgagctag aagacgagta ccaagaattg atccaaaaag 240

tgtatgtacc agtaggataa gcgatgacat ttcctttatt tgagacgac gctattgtga 300

acgggtgaaat tcagcacctt gccctgcac aacaacgta tgcggcaagt ttggcgacct 360

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cacttgaaca cactcaacat gcgcgataa tccgttgtcg gattgattac aatcagcaag 480

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gcagtattgg taatctgggtg tttcgccaag gtgagcaatg gttcacgcca gatagcccgt 720

tattttacgg cacacaacga gcctgggttat tacaacaagg caaaattcaa gcccggtcca 780

tcttattgca agagatcgca caatttgaag aaattcggtt aattaatgca ctaaatccgc 840

tgtaaatttt ccttgaacag cgtaaaataa aacaactttt tcagtcagat aaaaggagat 900

aaacgac atg acg aaa gta att cat act gac aat gca cca gcc gcc att 949

Met Thr Lys Val Ile His Thr Asp Asn Ala Pro Ala Ala Ile  
 1 5 10

ggg cct tat gta caa gcg gta gat tta ggt aat atg ctg tta acc tct 997

Gly Pro Tyr Val Gln Ala Val Asp Leu Gly Asn Met Leu Leu Thr Ser  
 15 20 25 30

ggg caa att cca gtg aat cca aaa acc ggt gaa gtg cca gcg gat atc 1045

Gly Gln Ile Pro Val Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Ile

| 35   | 40  | 45  |      |
|--|-----|-----|------|
| gta gca caa gca cgt caa tcg tta gaa aac gtg aaa gcg att gtg gaa    |     |     | 1093 |
| Val Ala Gln Ala Arg Gln Ser Leu Glu Asn Val Lys Ala Ile Val Glu    |     |     |      |
| 50   | 55  | 60  |      |
| caa gcg gga tta caa gtc gca aat atc gtg aaa acc acg gtg ttt gtg    |     |     | 1141 |
| Gln Ala Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val    |     |     |      |
| 65   | 70  | 75  |      |
| aaa gat tta aat gac ttt gca g g gtc aat gcg gag tat gaa cgt ttc    |     |     | 1189 |
| Lys Asp Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe    |     |     |      |
| 80   | 85  | 90  |      |
| ttt aaa gag aac aat cac cct agc ttc cct gct cgt tca tgt gtg gaa    |     |     | 1237 |
| Phe Lys Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu    |     |     |      |
| 95   | 100 | 105 | 110  |
| gtg gca cgt ttg ccg aaa gat gtg ggg att gaa atc gag gca atc gct    |     |     | 1285 |
| Val Ala Arg Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala    |     |     |      |
| 115  | 120 | 125 |      |
| gta aaa gcc taatgaatag cttgcattta tcttagtcgt agcaaaacaa            |     |     | 1334 |
| Val Lys Ala  |     |     |      |
| tctcttttca cttgctctct tcaaagcaag ttgataagtg atttttattg ggcgtttttc  |     |     | 1394 |
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| gagattctac aataccgttt aaaaccacaa tcaggacaaa cgtttcacca aattatgcgt  |     |     | 1514 |
| gagatcagtg ttccactcca taaacaacat gggattgatg tcattgcgta tggaaattca  |     |     | 1574 |
| ttacatgata ttgacagcta ttatttaatc cgtgcatttg agacagaaac caaattgcaa  |     |     | 1634 |
| cagcagctcg atgcttttta tgccagtgat gattggcgtg atggaccaag agaaagtatc  |     |     | 1694 |
| attcgctga ttgaaagcag tttaaaatcg gtgatcatgc tcccgacaca ggcaatccat   |     |     | 1754 |
| gcactacgca accattatcc tcaataaaat caacaaccgc acccaatcag tgcggtcatt  |     |     | 1814 |
| ttttcttact ttttcagtgc taagggaaaa acaacgatag tggacgttgt ttaatcaatt  |     |     | 1874 |
| tccaaacaca ttgcgcgata tcacaccaac tctcaatttc tgtttctaaa gaacgcagcg  |     |     | 1934 |
| caaccataa cgcgataaag aaactgacaa tcaaattcac cataccaatc aataacacga   |     |     | 1994 |
| acactaaacc ttgtaagaac atctgccaaag taaacgcgcc actgatcgcc atatagccca |     |     | 2054 |
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| cagaaataat ccagaaaaag aataaccaga aaccgcgaat ggcggcaaac cataaggacc  |     |     | 2354 |
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| taccaacata atgttgatag cctagcgcaa gcaacaagc cacagaaatc gctaaagtga   |     |     | 2474 |

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Ile Pro Val Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Ile Val Ala  
35 40 45  
Gln Ala Arg Gln Ser Leu Glu Asn Val Lys Ala Ile Val Glu Gln Ala  
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Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val Lys Asp  
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Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe Phe Lys  
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<222> (463)..(1884)

<220>  
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| Tyr | Asp | Ser | Ser | Lys | Met | Ala | Asp | Leu | Leu | Asn | Ser | Thr | His | Gly | Leu | 20  | 25  | 30  |    |
| Glu | Leu | Thr | Glu | Ile | Pro | Glu | Glu | Ala | Asp | Val | Leu | Leu | Leu | Asn | Thr | 35  | 40  | 45  |    |
| Cys | Ser | Ile | Arg | Glu | Lys | Ala | Gln | Glu | Lys | Val | Phe | His | Gln | Leu | Gly | 50  | 55  | 60  |    |
| Arg | Trp | Lys | Glu | Leu | Lys | Lys | His | Lys | Pro | Gly | Leu | Val | Ile | Gly | Val | 65  | 70  | 75  | 80 |
| Gly | Gly | Cys | Val | Ala | Ser | Gln | Glu | Gly | Glu | His | Ile | Arg | Thr | Arg | Ala | 85  | 90  | 95  |    |
| Pro | Tyr | Val | Asp | Ile | Ile | Phe | Gly | Pro | Gln | Thr | Leu | His | Arg | Leu | Pro | 100 | 105 | 110 |    |
| Glu | Met | Ile | Asn | Gln | Ile | Arg | Gly | Gly | Lys | Ser | Ser | Val | Val | Asp | Val | 115 | 120 | 125 |    |
| Ser | Phe | Pro | Glu | Ile | Glu | Lys | Phe | Asp | Arg | Leu | Pro | Glu | Pro | Arg | Ala | 130 | 135 | 140 |    |

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| 200   | 205 | 210 |      |
| gcg aaa ggc atg tta ggt aaa cat tac cgt tta ggt tgg gaa gag aaa     |     |     | 1087 |
| Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp Glu Glu Lys     |     |     |      |
| 215   | 220 | 225 |      |
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<211> 250

<212> PRT

<213> *Pasteurella multocida*

<400> 83

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| Met | Lys | Lys | Thr | Val | Val | Asn | Pro | Glu | Arg | Arg | Arg | Phe | Phe | Lys | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Thr | Arg | Thr | Ala | Gly | Gly | Leu | Ala | Gly | Val | Thr | Leu | Leu | Leu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Gln | Gln | Lys | Gln | Ser | Leu | Ala | Arg | Glu | Gly | Val | Ala | Leu | Arg | Pro |
|     | 35  |     |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Phe | Ala | Leu | Glu | Asn | Glu | Lys | Ala | Phe | Ser | Ala | Ala | Cys | Ile | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Gly | Gln | Cys | Val | Gln | Ala | Cys | Pro | His | Glu | Met | Leu | His | Leu | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Leu | Ile | Ser | Pro | Met | Glu | Ala | Gly | Thr | Pro | Tyr | Phe | Ile | Ala | Arg |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Lys | Pro | Cys | Glu | Met | Cys | Val | Asp | Ile | Pro | Cys | Ala | Lys | Ala | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Thr | Gly | Ala | Leu | Asp | Asn | Gln | Ala | Thr | Glu | Ile | Asp | Asp | Ala | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Met | Gly | Leu | Ala | Val | Leu | Leu | Asp | His | Glu | Thr | Cys | Leu | Asn | Trp | Gln |
|     | 130 |     |     |     |     |     | 135 |     |     |     | 140 |     |     |     |     |
| Gly | Leu | Arg | Cys | Asp | Val | Cys | Tyr | Arg | Val | Cys | Pro | Leu | Ile | Asn | Lys |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ala | Ile | Thr | Leu | Val | Met | His | Arg | Asn | Glu | Arg | Thr | Gly | Lys | His | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

Val Phe Ile Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys  
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Cys Glu Glu Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro  
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Met Ala Leu Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp  
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Glu Glu Lys Glu Lys Ala Gly His Ser Leu Ala Pro Glu Gly Ile Ile  
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Ser Leu Pro Thr Arg Leu Pro Glu Ser Leu  
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Leu Ser Tyr Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr
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atg agt att cat ttt gat aca tta aat aat aac gct gtt cgc ttt ctc 2545
Met Ser Ile His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu
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tca ggg ggc agc gtt ttt att tta gcc tgt ttt ttt tat tat cgc gct 2593
Ser Gly Gly Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala
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Glu Leu Thr Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro  
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 Ser Ser Ser Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser  
                     80                    85                    90  
 tac gtt aca atc tca aca ctt aat cgc gtt tgaccttccg atttttgata 2739  
 Tyr Val Thr Ile Ser Thr Leu Asn Arg Val  
                     95                    100  
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 gtcagaataa gtactgccgg tatatcgtct taatctaaga ttaagcttgc cacttttgtt 2859  
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&lt;210&gt; 85

&lt;211&gt; 103

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 85

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 Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr Met Ser Ile  
                     20                    25                    30  
 His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu Ser Gly Gly  
                     35                    40                    45  
 Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala Glu Leu Thr  
                     50                    55                    60  
 Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro Ser Ser Ser  
   65                    70                    75                    80  
 Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser Tyr Val Thr  
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<212> DNA  
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19

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18

<210> 90  
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<212> DNA  
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<400> 91  
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<210> 94  
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 <212> DNA  
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<220>  
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<210> 99  
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<210> 100  
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ggt aat gct gta ctc aaa cgt ttc tta gaa aca gat att cga gaa att 96
Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile
          20             25             30

cgt gtt ttt tcg cgt gat gag aag aaa caa gat gac atg cgg aaa aaa 144
Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys
          35             40             45

tat aat gat gca aaa tta aaa ttt tat att ggc gat gtt cgt gac tac 192
Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr
          50             55             60

gat agt att tta aat gcc tcg cga ggt gtt gac tat att tat cat gct 240
Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala
  65             70             75             80

gcc gca tta aag caa gtg cct tca tgc gag ttt tat ccg tta gag gca 288
Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala
          85             90             95

gtg aaa acc aat att tta ggt acg gca aat gtc tta gaa gcc gcc atc 336
Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile
          100             105             110

caa aac cag ata aaa cgc gtc gtc tgt ctt agc aca gat aaa gcg gtg 384
Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val
          115             120             125

tac cca att aat gcg atg ggc att tct aaa gca atg atg gaa aaa gtc 432
Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val
          130             135             140

atc atc gca aaa tcg cgt aac cta gaa ggc aca cca acg aca atc tgt 480
Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys
          145             150             155             160

tgt act cgc tat ggc aat gtc atg gca tcg cgt ggt tcg gtt atc cca 528
Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro
          165             170             175

tta ttt gtc gat caa ata cgt caa ggc aag cct ttt act att act gat 576
Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp
          180             185             190

cct gag atg aca cgc ttt atg atg aca ttg gaa gat gct gtg gat tta 624
Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu
          195             200             205

gtc cta tat gca ttt aaa aat ggt caa aat ggt gat gtt ttt gta caa 672
Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln
          210             215             220

aaa gcc ccc gca gca acc att ggt acc ctt gcc aaa gca att acc gaa 720
Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu
          225             230             235             240

tta tta tct gtc cca aat cac cct att tcc att ata ggt acg cgt cat 768
Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His

```

| 245   | 250 | 255 |      |
|---|-----|-----|------|
| gga gag aaa gca ttc gaa gct tta tta agc cgt gaa gaa atg gtt cat |     |     | 816  |
| Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His |     |     |      |
| 260   | 265 | 270 |      |
| gca att aat gaa ggt aat tat tat cgc atc cca gcc gat caa cgc agt |     |     | 864  |
| Ala Ile Asn Glu Gly Asn Tyr Tyr Arg Ile Pro Ala Asp Gln Arg Ser |     |     |      |
| 275   | 280 | 285 |      |
| tta aat tac agt aaa tat gtc gaa aaa ggg gaa cca aaa att acc gaa |     |     | 912  |
| Leu Asn Tyr Ser Lys Tyr Val Glu Lys Gly Glu Pro Lys Ile Thr Glu |     |     |      |
| 290   | 295 | 300 |      |
| gtc acc gac tac aac tca cat aat act gag cgt ttg act gtc aag gaa |     |     | 960  |
| Val Thr Asp Tyr Asn Ser His Asn Thr Glu Arg Leu Thr Val Lys Glu |     |     |      |
| 305   | 310 | 315 | 320  |
| atg aag cag tta ctg ctt aaa ctt gaa ttc ata cag aaa atg att gag |     |     | 1008 |
| Met Lys Gln Leu Leu Leu Lys Leu Glu Phe Ile Gln Lys Met Ile Glu |     |     |      |
| 325   | 330 | 335 |      |
| ggt gaa tac atc tca ccg gag gta ta                              |     |     | 1034 |
| Gly Glu Tyr Ile Ser Pro Glu Val                                 |     |     |      |
| 340   |     |     |      |
| <210> 101   |     |     |      |
| <211> 344   |     |     |      |
| <212> PRT   |     |     |      |
| <213> Pasteurella multocida                                     |     |     |      |
| <400> 101   |     |     |      |
| Met Phe Lys Asn Lys Thr Leu Leu Ile Thr Gly Gly Thr Gly Ser Phe |     |     |      |
| 1   | 5   | 10  | 15   |
| Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile |     |     |      |
| 20  | 25  | 30  |      |
| Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys |     |     |      |
| 35  | 40  | 45  |      |
| Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr |     |     |      |
| 50  | 55  | 60  |      |
| Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala |     |     |      |
| 65  | 70  | 75  | 80   |
| Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala |     |     |      |
| 85  | 90  | 95  |      |
| Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile |     |     |      |
| 100   | 105 | 110 |      |
| Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val |     |     |      |
| 115   | 120 | 125 |      |
| Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val |     |     |      |
| 130   | 135 | 140 |      |
| Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys |     |     |      |
| 145   | 150 | 155 | 160  |

Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro  
 165 170 175  
 Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp  
 180 185 190  
 Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu  
 195 200 205  
 Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln  
 210 215 220  
 Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu  
 225 230 235 240  
 Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His  
 245 250 255  
 Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His  
 260 265 270  
 Ala Ile Asn Glu Gly Asn Tyr Tyr Arg Ile Pro Ala Asp Gln Arg Ser  
 275 280 285  
 Leu Asn Tyr Ser Lys Tyr Val Glu Lys Gly Glu Pro Lys Ile Thr Glu  
 290 295 300  
 Val Thr Asp Tyr Asn Ser His Asn Thr Glu Arg Leu Thr Val Lys Glu  
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 Met Lys Gln Leu Leu Leu Lys Leu Glu Phe Ile Gln Lys Met Ile Glu  
 325 330 335  
 Gly Glu Tyr Ile Ser Pro Glu Val  
 340

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<220>  
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 <222> 1632  
 <223> Xaa = any or unknown amino acid

<400> 102  
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 Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Gln Val Lys Gly Cys  
 1 5 10 15  
 ctc gtt cct gtg gca gaa tgt att aac tca gct att agc aat ggt tca 96  
 Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser

| 20  | 25 | 30 |     |
|---|----|----|-----|
| tct gat tca aca tcc aca tca gaa caa gtt gaa gag gaa cct ttc ctt<br>Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu<br>35 40 45        |    |    | 144 |
| cta gaa caa tat tca ctt tcc tcc gtg tct tta tta gta aaa agc acg<br>Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr<br>50 55 60        |    |    | 192 |
| ttc aat cct gtt tgc tat gca atg caa ttg act tgg aaa cag ctt tct<br>Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser<br>65 70 75 80     |    |    | 240 |
| att tta ttt tta act gtg att tct gtt cct gtt ttg gct gag gga aaa<br>Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys<br>85 90 95        |    |    | 288 |
| ggg gat gaa aga aat caa tta aca gtg att gat aat agc gat cat att<br>Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile<br>100 105 110     |    |    | 336 |
| aaa tta gat gca tct aat ctt gct ggt aat gat aaa aca aaa atc tat<br>Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr<br>115 120 125     |    |    | 384 |
| caa gca gaa aat aaa gtt ctg gtt att gat att gct aaa cca aat ggg<br>Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly<br>130 135 140     |    |    | 432 |
| aaa ggg att tca gat aac cgt ttt gaa aaa ttt aat att cca aat agc<br>Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser<br>145 150 155 160 |    |    | 480 |
| gcg gtg ttt aat aat aat ggg act gaa gcg cag gca aga tca aca tta<br>Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu<br>165 170 175     |    |    | 528 |
| att ggt tac att ccg caa aat caa aat tta agg gga ggg aaa gaa gct<br>Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala<br>180 185 190     |    |    | 576 |
| gat gtt ata tta aat caa gtg aca ggt cct caa gaa agt aaa att gtt<br>Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val<br>195 200 205     |    |    | 624 |
| ggc gcg ctt gaa gta tta ggt aaa aaa gct gat atc gtc att gca aac<br>Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn<br>210 215 220     |    |    | 672 |
| caa aat ggt att acc tta aat ggt gta aga aca ata aat tca gat cgt<br>Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg<br>225 230 235 240 |    |    | 720 |
| ttt gtt gcc act acg agt gag ctt ata gat ccg aat cag atg atg tta<br>Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu<br>245 250 255     |    |    | 768 |
| aag gtt aca aaa gga aat gtg atc att gat att gat ggt ttt tgc aca<br>Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr<br>260 265 270     |    |    | 816 |
| gat gga tta aag tat tta gat att att gct aaa aaa att gaa caa aag   |    |    | 864 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Asp | Gly | Leu | Lys | Tyr | Leu | Asp | Ile | Ile | Ala | Lys | Lys | Ile | Glu | Gln | Lys |      |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |
| caa | tca | att | aca | tca | ggg | gat | aat | tca | gaa | gca | aaa | aca | gat | gtc | act | 912  |
| Gln | Ser | Ile | Thr | Ser | Gly | Asp | Asn | Ser | Glu | Ala | Lys | Thr | Asp | Val | Thr |      |
|     |     | 290 |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |
| ctt | att | gcg | ggg | tcc | agt | gaa | tat | gat | tta | agc | aaa | cat | gag | ctg | aaa | 960  |
| Leu | Ile | Ala | Gly | Ser | Ser | Glu | Tyr | Asp | Leu | Ser | Lys | His | Glu | Leu | Lys |      |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |      |
| aaa | acg | agc | ggg | gaa | aat | gta | tct | aat | gat | gtt | att | gct | atc | acg | gga | 1008 |
| Lys | Thr | Ser | Gly | Glu | Asn | Val | Ser | Asn | Asp | Val | Ile | Ala | Ile | Thr | Gly |      |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |      |
| tct | agt | aca | ggc | gca | atg | cat | ggg | aaa | aat | att | aag | ttg | att | gtg | aca | 1056 |
| Ser | Ser | Thr | Gly | Ala | Met | His | Gly | Lys | Asn | Ile | Lys | Leu | Ile | Val | Thr |      |
|     |     |     | 340 |     |     |     | 345 |     |     |     |     |     | 350 |     |     |      |
| gat | aaa | ggg | gca | ggc | gta | aaa | cat | gat | gga | att | att | ttg | tct | gaa | aat | 1104 |
| Asp | Lys | Gly | Ala | Gly | Val | Lys | His | Asp | Gly | Ile | Ile | Leu | Ser | Glu | Asn |      |
|     |     | 355 |     |     |     | 360 |     |     |     |     |     | 365 |     |     |     |      |
| gat | att | cag | att | gaa | atg | aat | gaa | ggg | gac | tta | gaa | ctt | ggc | aat | acg | 1152 |
| Asp | Ile | Gln | Ile | Glu | Met | Asn | Glu | Gly | Asp | Leu | Glu | Leu | Gly | Asn | Thr |      |
|     |     | 370 |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |
| att | cag | caa | aca | gtg | gta | aaa | aaa | gac | cga | aat | att | cga | gcc | aag | aaa | 1200 |
| Ile | Gln | Gln | Thr | Val | Val | Lys | Lys | Asp | Arg | Asn | Ile | Arg | Ala | Lys | Lys |      |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |      |
| aaa | att | gaa | gtg | aaa | aac | gct | aat | cgt | gtt | ttt | gtt | ggg | agt | caa | acg | 1248 |
| Lys | Ile | Glu | Val | Lys | Asn | Ala | Asn | Arg | Val | Phe | Val | Gly | Ser | Gln | Thr |      |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |      |
| aaa | tca | gat | gaa | att | tcg | tta | gag | gcg | aaa | caa | gtt | aaa | atc | aga | aaa | 1296 |
| Lys | Ser | Asp | Glu | Ile | Ser | Leu | Glu | Ala | Lys | Gln | Val | Lys | Ile | Arg | Lys |      |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |      |
| aac | gca | gag | att | agg | agt | acg | aca | caa | gcc | aaa | atc | gta | gca | aag | ggg | 1344 |
| Asn | Ala | Glu | Ile | Arg | Ser | Thr | Thr | Gln | Ala | Lys | Ile | Val | Ala | Lys | Gly |      |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |      |
| gcc | ctg | tct | att | gag | caa | aat | gcg | aag | ctc | gtc | gct | aaa | aag | ata | gat | 1392 |
| Ala | Leu | Ser | Ile | Glu | Gln | Asn | Ala | Lys | Leu | Val | Ala | Lys | Lys | Ile | Asp |      |
|     |     | 450 |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |      |
| gtg | gca | aca | gaa | act | cta | act | aat | gct | ggg | cgt | att | tat | ggg | cga | gag | 1440 |
| Val | Ala | Thr | Glu | Thr | Leu | Thr | Asn | Ala | Gly | Arg | Ile | Tyr | Gly | Arg | Glu |      |
| 465 |     |     |     |     | 470 |     |     |     | 475 |     |     |     |     |     | 480 |      |
| gtt | aag | ctt | gac | act | aat | aat | ttg | att | aat | gat | aaa | gaa | att | tat | gct | 1488 |
| Val | Lys | Leu | Asp | Thr | Asn | Asn | Leu | Ile | Asn | Asp | Lys | Glu | Ile | Tyr | Ala |      |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |      |
| gaa | cgg | aaa | ttg | agt | att | ttg | acg | aaa | gga | aaa | gat | ctt | gaa | att | att | 1536 |
| Glu | Arg | Lys | Leu | Ser | Ile | Leu | Thr | Lys | Gly | Lys | Asp | Leu | Glu | Ile | Ile |      |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |      |
| caa | gat | aga | tat | ttg | tct | cca | ctg | atg | cgc | gta | aaa | agt | agt | gtc | cgc | 1584 |
| Gln | Asp | Arg | Tyr | Leu | Ser | Pro | Leu | Met | Arg | Val | Lys | Ser | Ser | Val | Arg |      |
|     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |      |

|   |      |
|---|------|
| ttt tta ggc tct ccg ttt ttc tca ata tct ccg tcg atg ctc gca agc | 1632 |
| Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser |      |
| 530 535 540   |      |
| ctt agt gca cag ttt aag cct ggt ttt gtg aat aag gga ctc att gaa | 1680 |
| Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu |      |
| 545 550 555 560   |      |
| agt gcg ggg agt gca gaa tta act ttt aaa gaa aaa acc agt ttt tta | 1728 |
| Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu |      |
| 565 570 575   |      |
| aca gag ggc aat aat ttt att aga gct aaa gat gcg tta act att aac | 1776 |
| Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn |      |
| 580 585 590   |      |
| gcc caa aat att gaa att gat aaa aat caa gat att caa ttg ggt gct | 1824 |
| Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala |      |
| 595 600 605   |      |
| aat ata acg ttg aat gtg gaa gaa aac ttt gtt aat cgt gca gga aca | 1872 |
| Asn Ile Thr Leu Asn Val Glu Asn Phe Val Asn Arg Ala Gly Thr     |      |
| 610 615 620   |      |
| ctg gca act ggt aaa aca ctg aca att aat acc gaa agt ggc agt att | 1920 |
| Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile |      |
| 625 630 635 640   |      |
| tac aat ctt ggt ggg aca tta ggt gct gga aaa tca tta aaa ctg act | 1968 |
| Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr |      |
| 645 650 655   |      |
| gct aaa tca acg gaa gaa ggt atg gga aat att gtt aac caa gaa aac | 2016 |
| Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn |      |
| 660 665 670   |      |
| ggt tta ttc cat aca ctc ggt aat atg atg tta gaa gca gag cgt tct | 2064 |
| Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser |      |
| 675 680 685   |      |
| gtt tat aat att ggc gat att tat gcg agt aaa aaa tta aca gtt cat | 2112 |
| Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His |      |
| 690 695 700   |      |
| act cat aat ttg att aat gat gtg cgt tta tct ggc aat gtg agt tat | 2160 |
| Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr |      |
| 705 710 715 720   |      |
| aag cct atc ggt tca agt cgt gat tat gat atc agt cgt gtt gcg gta | 2208 |
| Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val |      |
| 725 730 735   |      |
| cat ggt tgg cac aat aat gtt tat aag ctc aac tta aat ctg caa gaa | 2256 |
| His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu |      |
| 740 745 750   |      |
| caa gat aaa acc gat att aaa gtt gtg aaa atg ggg gct atc cgt tct | 2304 |
| Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser |      |
| 755 760 765   |      |
| gat ggt gat ttt gac ttt aag gga ata aag gcg aca tca tca gaa tca | 2352 |
| Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser |      |
| 770 775 780   |      |



|   |      |
|---|------|
| aaa ccg cag tta att aat cat gga tta att aat gtc aaa gga aca ttt | 2400 |
| Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe |      |
| 785 790 795 800   |      |
| aat gcg gaa gct gat caa gtg gtg aac caa atg aaa gcg ttt aac caa | 2448 |
| Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln |      |
| 805 810 815   |      |
| aat gca tta gca agc gtg ttt aag aat cca gcg aaa atc acg atg tac | 2496 |
| Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr |      |
| 820 825 830   |      |
| tat caa cca ctt act cgt tat att tgg aca cca tta tcg ggt aat gca | 2544 |
| Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala |      |
| 835 840 845   |      |
| tcg cgt gaa ttt aac aat tta gag tct ttc ctc gat gcc ttg ttt ggc | 2592 |
| Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly |      |
| 850 855 860   |      |
| tca aca aca atc tta aaa tca agt ttc tat agt acg gaa aat ttt agt | 2640 |
| Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser |      |
| 865 870 875 880   |      |
| gct tat cag ctt cta tct cat att cag cat tca cca atg tac caa aaa | 2688 |
| Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys |      |
| 885 890 895   |      |
| gcg atg gca caa gtg ttt ggt gca gag tgg cat agt aaa tcc tat gat | 2736 |
| Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp |      |
| 900 905 910   |      |
| gag atg cga aac aaa tgg aaa agc ttt aaa gaa aat cca aca gat ttc | 2784 |
| Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe |      |
| 915 920 925   |      |
| att tat tac cca tca gaa aaa gca aaa atc cta gcg gga aaa cta gaa | 2832 |
| Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu |      |
| 930 935 940   |      |
| ggt aag ctt aca acg cta caa aat ggt gaa tat gcc gaa cgt ggt aag | 2880 |
| Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys |      |
| 945 950 955 960   |      |
| ttt gat gag agt atc caa att ggt aaa cac caa tta tcg cta cca tca | 2928 |
| Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser |      |
| 965 970 975   |      |
| gta gag ctt aaa gcg gag ttt agt gat aaa gaa cgt ttg gaa gag gac | 2976 |
| Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp |      |
| 980 985 990   |      |
| ggg gta gat tta tcc tcg atc gcc gaa ctc tta gaa atg cca aac tta | 3024 |
| Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu |      |
| 995 1000 1005   |      |
| ttt att gat aat agt atc caa tta gaa aag aaa aag ttg tct cct att | 3072 |
| Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile |      |
| 1010 1015 1020  |      |
| gag gat cta gat gaa gaa cca cgt aaa aat ctg gat ata gaa gaa agc | 3120 |
| Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser |      |
| 1025 1030 1035 1040   |      |

|   |      |
|---|------|
| cat tct aat tca tgc gat gac gtg ctt agc atg aat gat gat gag tct | 3168 |
| His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser |      |
| 1045 1050 1055  |      |
| gat aca gac gat agc aag tgg agt atg ggc aat gat gag aaa gag atg | 3216 |
| Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met |      |
| 1060 1065 1070  |      |
| ccc gat gat aag ctg ggt ata agt cgt gat gat cgt gga aat aaa cca | 3264 |
| Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro |      |
| 1075 1080 1085  |      |
| cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa ttc ttt | 3312 |
| Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe |      |
| 1090 1095 1100  |      |
| gaa aat ggt tat ctc ttg aat gag cta cta cag gag ctt gga gaa gag | 3360 |
| Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu |      |
| 1105 1110 1115 1120   |      |
| ccg tta cta aaa gaa ggg gaa gat cat ttt aaa cgt tct acc aat cta | 3408 |
| Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu |      |
| 1125 1130 1135  |      |
| gtc cgt cta ggc gag aga gat agg caa aat aga gaa aag aga gaa aaa | 3456 |
| Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys |      |
| 1140 1145 1150  |      |
| gag ggg tat ttt gat ctg cct ggt aca tta gat atg aaa ctg cag gag | 3504 |
| Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu |      |
| 1155 1160 1165  |      |
| tta ttc gaa aaa aga aaa caa aaa cac gaa gca gaa cag aaa gca aga | 3552 |
| Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg |      |
| 1170 1175 1180  |      |
| ata gaa aaa gca ctt cta caa aaa tca gaa caa caa gaa aaa cgt gtt | 3600 |
| Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val |      |
| 1185 1190 1195 1200   |      |
| gaa gaa cgt aag caa gag gaa aaa cgt caa gcg caa gat aaa att gct | 3648 |
| Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala |      |
| 1205 1210 1215  |      |
| aag caa gta gaa att gca aaa gaa atg caa cgg gta gaa gaa att cgc | 3696 |
| Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg |      |
| 1220 1225 1230  |      |
| cag aga gaa aaa caa ctt gcg atc caa ctg caa gaa gaa gag aag aaa | 3744 |
| Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu Lys Lys |      |
| 1235 1240 1245  |      |
| caa caa gaa gaa aaa cat tta tcc gag gag aaa aaa caa gct gaa cag | 3792 |
| Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln |      |
| 1250 1255 1260  |      |
| aaa caa aaa gct gag gag aaa gtt gca caa gaa aga tta gac att gaa | 3840 |
| Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu |      |
| 1265 1270 1275 1280   |      |
| caa cag aaa gcg tat gaa gaa atg gcg aag cga gag gca gag gca tca | 3888 |
| Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser |      |
| 1285 1290 1295  |      |

|   |      |
|---|------|
| aaa aat gtt tta ttg aaa gcg att gat gaa gaa cgt cca aaa gtg gaa | 3936 |
| Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu |      |
| 1300 1305 1310  |      |
| act gat cca ctt ttc cgt aca aaa ttg aaa tat atc aat caa gat gac | 3984 |
| Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp |      |
| 1315 1320 1325  |      |
| tat gct ggt gca aat tat ttc ttc aat aaa gtt ggt tta aat aca aaa | 4032 |
| Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys |      |
| 1330 1335 1340  |      |
| ggt cat caa aaa gta aat gtg tta ggg gat aac tat ttt gat cat caa | 4080 |
| Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln |      |
| 1345 1350 1355 1360   |      |
| gtg att act cgc tcg att gag aaa aaa gta gat aac cac ctt aac caa | 4128 |
| Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln |      |
| 1365 1370 1375  |      |
| aaa tac aat ctc agc gat gtg gaa tta gtt aaa cag ctg atg gac aat | 4176 |
| Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn |      |
| 1380 1385 1390  |      |
| tcc aca aca caa gcg cag gag ttg gat ttg aaa cta ggt gcg gca tta | 4224 |
| Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu |      |
| 1395 1400 1405  |      |
| act aaa gaa caa caa gct aac ttg acc caa gat atc gtt tgg tat gtc | 4272 |
| Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val |      |
| 1410 1415 1420  |      |
| aaa acg aag gta aag ggc aaa gat gtg ttt gtt cca aag gtt tat ttc | 4320 |
| Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe |      |
| 1425 1430 1435 1440   |      |
| gct tct gaa acg ctc gta gaa gcc caa aaa tta caa ggt tta ggc act | 4368 |
| Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr |      |
| 1445 1450 1455  |      |
| ggg act atc aga gtt ggt gaa gct aag att aaa gcc aaa gat gtg gtg | 4416 |
| Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val |      |
| 1460 1465 1470  |      |
| aat acc ggg aca tta gct ggg aga aaa ctc aat gtt gaa gcg agt aat | 4464 |
| Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn |      |
| 1475 1480 1485  |      |
| aaa atc aaa aat caa ggg agt atc tta agt act caa gaa aca cgt tta | 4512 |
| Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu |      |
| 1490 1495 1500  |      |
| gtc ggg cgt aaa ggt att gaa aac gta tct cgt tca ttt gca aat gat | 4560 |
| Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp |      |
| 1505 1510 1515 1520   |      |
| gaa tta gga gtc act gca caa cgc tca gaa atc aaa acg gaa ggt cat | 4608 |
| Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His |      |
| 1525 1530 1535  |      |
| tta cat ctt gaa aca gat aag gat tca act att gat gta caa gca tcg | 4656 |
| Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser |      |
| 1540 1545 1550  |      |

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gat att aaa gca aaa aca agc ttt gtg aag act ggt gat gtg aat ctc 4704
Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu
      1555                      1560                      1565

aaa aat aca tac aat act aaa cat gcc tac cgt gag aaa ttc tcg ccg 4752
Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro
      1570                      1575                      1580

agt gca cta caa gtt gca gaa ctt gat gtg gca ggg ctt aaa gtc cca 4800
Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
      1585                      1590                      1595                      1600

ctt tta ggc gtg tcc gtc tcc atc cag ttt att cag agc ata cta gtg 4848
Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val
      1605                      1610                      1615

agg caa ctt caa gag gga tca atc ttc gaa gta ggg cac tta cat ntt 4896
Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa
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gcg gta gac aga aga tgt gaa cca agc ggg gag ta 4931
Ala Val Asp Arg Arg Cys Glu Pro Ser Gly Glu
      1635                      1640

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&lt;210&gt; 103

&lt;211&gt; 1643

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 1632

&lt;223&gt; Xaa = any or unknown amino acid

&lt;400&gt; 103

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Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu
      35              40              45

Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
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Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
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Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys
      85              90              95

Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile
      100              105              110

Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
      115              120              125

Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly
      130              135              140

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Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser  
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 Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu  
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 Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala  
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 Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val  
 195 200 205  
 Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn  
 210 215 220  
 Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg  
 225 230 235 240  
 Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu  
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 Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr  
 260 265 270  
 Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys  
 275 280 285  
 Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr  
 290 295 300  
 Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys  
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 Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly  
 325 330 335  
 Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr  
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 Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn  
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 Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr  
 370 375 380  
 Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys  
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 Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr  
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 Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys  
 420 425 430  
 Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly  
 435 440 445  
 Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp  
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 Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu  
 465 470 475 480

Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala  
 485 490 495  
 Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile  
 500 505 510  
 Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg  
 515 520 525  
 Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser  
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 Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu  
 565 570 575  
 Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn  
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 Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala  
 595 600 605  
 Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr  
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 Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr  
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 660 665 670  
 Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser  
 675 680 685  
 Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His  
 690 695 700  
 Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr  
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 Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val  
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 His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu  
 740 745 750  
 Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser  
 755 760 765  
 Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser  
 770 775 780  
 Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe  
 785 790 795 800  
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 805 810 815

Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr  
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 Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala  
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 Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly  
                     850                    855                    860  
 Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser  
                     865                    870                    875                    880  
 Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys  
                     885                    890                    895  
 Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp  
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 Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe  
                     915                    920                    925  
 Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu  
                     930                    935                    940  
 Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys  
                     945                    950                    955                    960  
 Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser  
                     965                    970                    975  
 Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp  
                     980                    985                    990  
 Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu  
                     995                    1000                    1005  
 Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile  
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 Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser  
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 His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser  
                     1045                    1050                    1055  
 Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met  
                     1060                    1065                    1070  
 Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro  
                     1075                    1080                    1085  
 Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe  
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 Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu  
                     1105                    1110                    1115                    1120  
 Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu  
                     1125                    1130                    1135  
 Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys  
                     1140                    1145                    1150

Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu  
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 Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg  
 1170 1175 1180  
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 1285 1290 1295  
 Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu  
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 Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln  
 1345 1350 1355 1360  
 Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln  
 1365 1370 1375  
 Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn  
 1380 1385 1390  
 Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu  
 1395 1400 1405  
 Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val  
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 Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe  
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 1445 1450 1455  
 Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val  
 1460 1465 1470  
 Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn  
 1475 1480 1485



Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu  
 1490 1495 1500

Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp  
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Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His  
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Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser  
 1540 1545 1550

Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu  
 1555 1560 1565

Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro  
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Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro  
 1585 1590 1595 1600

Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val  
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ccg cag gct gaa tcg act ata tct act tcc gca cgt tat tcg act gaa 96  
 Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu  
 20 25 30

cgt cat aat ggt aat att aat aat att gaa tac gaa aat gtt agt tcg 144  
 Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser  
 35 40 45

ttg aaa gtt caa aaa ggg gca gct tct gta atg tat ggt agc ggt gcg 192  
 Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala  
 50 55 60

tta ggt gga acc gtg gag ttt acc aca aaa gat att gag gac ttt gtc 240  
 Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val  
 65 70 75 80

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| Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser |      |
| 85 90 95  |      |
| aaa aac aga gaa tat cgt caa gtc atc gga gtt gga ggg aaa ggg gaa | 336  |
| Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu |      |
| 100 105 110   |      |
| cac ttt ttt ggt ttt gta caa tta acc aaa cgt tgg ggg cat gaa aca | 384  |
| His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr |      |
| 115 120 125   |      |
| atc aac aac ggc aaa ggt aca gac att ctc ggc gaa cat cga ggt aaa | 432  |
| Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys |      |
| 130 135 140   |      |
| ccc aat ccg ctc aac tac tat act aca tca tgg tta acg aaa gtc ggt | 480  |
| Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly |      |
| 145 150 155 160   |      |
| tac gat att aat aac act cat cgt ttt aca ctg ttt tta gaa gat cgc | 528  |
| Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg |      |
| 165 170 175   |      |
| cgt gaa aag aag ctt acc gaa gaa aaa aca tta ggg ctt agt gat gca | 576  |
| Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala |      |
| 180 185 190   |      |
| gtg cgt ttt gct aat gat caa acc cct tat ctc cgt tat ggt att gaa | 624  |
| Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu |      |
| 195 200 205   |      |
| tat cga tat aac ggc ttg tct tgg ttg gaa acg gta aag ctt ttt ttg | 672  |
| Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu |      |
| 210 215 220   |      |
| gca aag cag aaa atc gaa caa cgt tct gct ctc caa gag ttt gat att | 720  |
| Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile |      |
| 225 230 235 240   |      |
| aat aat agg aat aaa ttg gat tcg act atg tcg ttt gta tat tta caa | 768  |
| Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln |      |
| 245 250 255   |      |
| aga cag aat ata gct cgg gga gaa ttt tca acg agt cct tta tat tgg | 816  |
| Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp |      |
| 260 265 270   |      |
| ggg ccg agt cgc cat cgt tta tct gcg aaa ttc gaa ttt cgt gat aag | 864  |
| Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys |      |
| 275 280 285   |      |
| ttt tta gaa aat atg aat aag cat ttt acg ttt cgg ccg tgg caa atc | 912  |
| Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile |      |
| 290 295 300   |      |
| aat aga ttc aga caa caa ggt cga aat aac tat aca gaa gtg ttt ccc | 960  |
| Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro |      |
| 305 310 315 320   |      |
| gtt aaa tcc cga gag ttt tct ttt tct ctt atg gac gac att aag att | 1008 |
| Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile |      |
| 325 330 335   |      |

|   |      |
|---|------|
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| Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg Trp Asp His Tyr Asn |      |
| 340 345 350   |      |
| tat aag cca tta tta aat tct cag cat aat atc aac agg aca cag aga | 1104 |
| Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg |      |
| 355 360 365   |      |
| tta cct tat cca aaa aca tca tcc aaa ttt tcg tat caa ttg agt tta | 1152 |
| Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu |      |
| 370 375 380   |      |
| gag tat caa tta cat cca tca cat caa att gca tac cgt tta agt acc | 1200 |
| Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr |      |
| 385 390 395 400   |      |
| ggt ttt agg gtt ccc cgt gtt gaa gat ctt tat ttt gaa gac cga gga | 1248 |
| Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly |      |
| 405 410 415   |      |
| aaa agt tct tca caa ttt ctt cct aac ccc gat cta caa ccg gaa act | 1296 |
| Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr |      |
| 420 425 430   |      |
| gca ctg aat cat gaa ata agt tac cgt ttc caa aat caa tat gcc cat | 1344 |
| Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His |      |
| 435 440 445   |      |
| ttc agc gtc ggg ctt ttc cgt aca cgt tat cat aac ttt att caa gaa | 1392 |
| Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu |      |
| 450 455 460   |      |
| cgt gag atg acc tgt gat aaa att cca tat gag tat aat agg act tat | 1440 |
| Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr |      |
| 465 470 475 480   |      |
| gga tat tgc acg cat aat act tat gta atg ttt gtt aat gaa cct gaa | 1488 |
| Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu |      |
| 485 490 495   |      |
| gcc gtg att aaa ggg gtt gaa gta agc ggt gct tta aat ggg tcg gca | 1536 |
| Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala |      |
| 500 505 510   |      |
| ttc gga ctt tcc gac ggt tta act ttc cgt ctc aaa ggg agc tac agc | 1584 |
| Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser |      |
| 515 520 525   |      |
| aaa ggt caa aat cat gac ggc gat ccg tta aaa tct att caa cca tgg | 1632 |
| Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp |      |
| 530 535 540   |      |
| aca gtg gta acc ggt att gat tac gaa act gaa ggg tgg agc gtg agt | 1680 |
| Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser |      |
| 545 550 555 560   |      |
| ttg agc ggg cgt tat agt gcg gct aaa aaa gcc aaa gat gcg ata gaa | 1728 |
| Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu |      |
| 565 570 575   |      |
| acg gaa tac aca cat gat aaa aag gtt gtc aaa caa tgg ccg cat tta | 1776 |
| Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu |      |
| 580 585 590   |      |

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agt cca tcc tac ttt gtt gtt gat ttt acg ggg caa gtt aac ctc agt 1824
Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser
      595                      600                      605

aaa aat gtc att ttg aat atg ggg gta ttt aac ttg ttc aat cgt gat 1872
Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp
      610                      615                      620

tat atg acg tgg gac agt gca tat aac ttg ttt act agg ggg tat act 1920
Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
      625                      630                      635                      640

tcc cgt tct gtc cgt gct aac agc cca ggc att aat cgg ttt acc gca 1968
Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
      645                      650                      655

cca aaa cgt aat ttt gct gcc tcg gtg gaa att cgt ttt ta 2009
Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
      660                      665

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&lt;210&gt; 105

&lt;211&gt; 669

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 105

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Ile Arg Gly Val Asp Lys Asp Arg Val Ala Val Ile Val Asp Gly Ile
  1                      5                      10                      15

Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
      20                      25                      30

Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
      35                      40                      45

Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
      50                      55                      60

Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
      65                      70                      75                      80

Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
      85                      90                      95

Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
      100                      105                      110

His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr
      115                      120                      125

Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys
      130                      135                      140

Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly
      145                      150                      155                      160

Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg
      165                      170                      175

Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala
      180                      185                      190

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Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu  
 195 200 205  
 Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu  
 210 215 220  
 Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile  
 225 230 235 240  
 Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln  
 245 250 255  
 Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp  
 260 265 270  
 Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys  
 275 280 285  
 Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile  
 290 295 300  
 Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro  
 305 310 315 320  
 Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile  
 325 330 335  
 Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg Trp Asp His Tyr Asn  
 340 345 350  
 Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg  
 355 360 365  
 Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu  
 370 375 380  
 Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr  
 385 390 395 400  
 Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly  
 405 410 415  
 Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr  
 420 425 430  
 Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His  
 435 440 445  
 Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu  
 450 455 460  
 Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr  
 465 470 475 480  
 Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu  
 485 490 495  
 Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala  
 500 505 510  
 Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser  
 515 520 525

Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp  
 530 535 540  
 Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser  
 545 550 555 560  
 Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu  
 565 570 575  
 Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu  
 580 585 590  
 Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser  
 595 600 605  
 Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp  
 610 615 620  
 Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr  
 625 630 635 640  
 Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala  
 645 650 655  
 Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe  
 660 665

<210> 106  
 <211> 908  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <223> lgtC  
 <220>  
 <221> CDS  
 <222> (1)..(906)

<400> 106  
 atg aat att tta ttt gtt tct gat gat gtt tat gct aaa cat ctg gtg 48  
 Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val  
 1 5 10 15  
 gtt gcg att aaa agc att ata aat cat aat gaa aaa ggt att tca ttt 96  
 Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe  
 20 25 30  
 tat att ttt gat ttg ggt ata aag gat gaa aat aag aga aat att aat 144  
 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn  
 35 40 45  
 gat att gtt tct tct tat gga agt gaa gtc aac ttt att gct gtg aat 192  
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn  
 50 55 60  
 gag aaa gaa ttt gag agt ttt cct gtt caa att agt tat att tct tta 240  
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu  
 65 70 75 80

gca aca tat gca agg cta aaa gcg gca gag tat ttg ccg gat aat tta 288  
 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu  
 85 90 95  
 aat aaa att att tat tta gat gtt gat gtt ttg gtt ttt aac tca tta 336  
 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu  
 100 105 110  
 gaa atg tta tgg aat gtt gat gtt aat aat ttt ctt acc gca gcc tgt 384  
 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys  
 115 120 125  
 tat gat tct ttc atc gaa aat gaa aag tct gag cat aaa aaa tcg att 432  
 Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile  
 130 135 140  
 tca atg tca gat aag gaa tat tat ttt aat gca gga gta atg cta ttt 480  
 Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe  
 145 150 155 160  
 aat tta gat gaa tgg cgg aag atg gat gta ttc tca aga gct tta gac 528  
 Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp  
 165 170 175  
 ctg tta gct atg tat cct aat caa atg att tat cag gat caa gat ata 576  
 Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile  
 180 185 190  
 ttg aat atc ctt ttt agg aat aaa gtc tgt tat tta gat tgc aga ttt 624  
 Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe  
 195 200 205  
 aat ttc atg cca aat caa ctt gaa aga ata aaa caa tac cat aaa gga 672  
 Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly  
 210 215 220  
 aaa ttg agc aac tta cat tct tta gaa aaa aca acg atg cct gtc gtt 720  
 Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val  
 225 230 235 240  
 att tca cat tat tgt ggt cca gaa aaa gcg tgg cat gcg gat tgt aaa 768  
 Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys  
 245 250 255  
 cat ttt aat gta tat ttc tat cag aaa ata tta gca gaa ata acg aga 816  
 His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg  
 260 265 270  
 ggc acg gat aaa gaa cgc gta tta tct ata aaa act tat ctc aag gcc 864  
 Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala  
 275 280 285  
 ttg att aga agg att aga tat aaa ttc aaa tat caa gtc tat ta 908  
 Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr  
 290 295 300

&lt;210&gt; 107

&lt;211&gt; 302

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 107

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Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
 1           5           10           15

Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
          20           25           30

Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
          35           40           45

Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
          50           55           60

Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
          65           70           75           80

Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
          85           90           95

Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
          100          105          110

Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
          115          120          125

Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
          130          135          140

Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
          145          150          155          160

Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
          165          170          175

Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
          180          185          190

Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
          195          200          205

Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly
          210          215          220

Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
          225          230          235          240

Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
          245          250          255

His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg
          260          265          270

Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala
          275          280          285

Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
          290          295          300

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&lt;210&gt; 108

&lt;211&gt; 2054

&lt;212&gt; DNA

&lt;213&gt; Pasteurella multocida



&lt;220&gt;

&lt;223&gt; pnp

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (2052)

&lt;400&gt; 108

|   |     |
|---|-----|
| atg gca agt atg gat gat act act gtg ttt gtc aca gtg gtt gcc aaa | 48  |
| Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys |     |
| 1 5 10 15   |     |
| aaa gat gtg aaa gaa ggt caa gac ttc ttc cca tta act gtt aac tat | 96  |
| Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr |     |
| 20 25 30  |     |
| caa gag cgt act tat gct gca ggc cgt att cct ggt ggc ttt ttc aaa | 144 |
| Gln Glu Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys |     |
| 35 40 45  |     |
| cgt gaa ggt cgt cct tct gaa ggc gaa act tta att gct cgt tta att | 192 |
| Arg Glu Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile |     |
| 50 55 60  |     |
| gac cgt cca att cgt cct ctt ttc cca gaa ggt ttt tat aac gaa atc | 240 |
| Asp Arg Pro Ile Arg Pro Leu Phe Pro Glu Gly Phe Tyr Asn Glu Ile |     |
| 65 70 75 80   |     |
| caa atc gtg gcg aca gtg gtg tct gtt aat ccg caa att tgt cca gat | 288 |
| Gln Ile Val Ala Thr Val Val Ser Val Asn Pro Gln Ile Cys Pro Asp |     |
| 85 90 95  |     |
| tta gtg gca atg atc ggt gca tct gcg gca ctt tct tta tca ggt gtg | 336 |
| Leu Val Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val |     |
| 100 105 110   |     |
| cca ttt aat ggc cct atc ggt gcg gca cgt gtt ggt ttt att gat gat | 384 |
| Pro Phe Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asp Asp |     |
| 115 120 125   |     |
| caa ttt gtg tta aac cca acc atg aac gag caa aaa caa agc cgt tta | 432 |
| Gln Phe Val Leu Asn Pro Thr Met Asn Glu Gln Lys Gln Ser Arg Leu |     |
| 130 135 140   |     |
| gac ttg gtt gtc gcg gga aca gat aaa gcg gtg tta atg gtg gaa tct | 480 |
| Asp Leu Val Val Ala Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser |     |
| 145 150 155 160   |     |
| gaa gcc gat gta tta acc gaa gaa caa atg tta gct gcg gtg gtg ttt | 528 |
| Glu Ala Asp Val Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe |     |
| 165 170 175   |     |
| ggt cat cag caa caa caa gtg gtg att gac gcg atc aaa gaa ttt acc | 576 |
| Gly His Gln Gln Gln Val Val Ile Asp Ala Ile Lys Glu Phe Thr     |     |
| 180 185 190   |     |
| gca gaa gcc ggt aaa ccg cgt tgg gat tgg gtg gca cct gaa cca aat | 624 |
| Ala Glu Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn |     |
| 195 200 205   |     |
| acc gcg tta att gaa aaa gtg aaa gcg att gca gaa gcg cgt tta ggc | 672 |
| Thr Ala Leu Ile Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly |     |
| 210 215 220   |     |

|   |      |
|---|------|
| gaa gca tac cgt atc act gaa aaa caa gca cgt tat gaa caa att gat | 720  |
| Glu Ala Tyr Arg Ile Thr Glu Lys Gln Ala Arg Tyr Glu Gln Ile Asp |      |
| 225 230 235 240   |      |
| gcg att aaa gct gat gtg att gca caa atc aca gct gaa gta gca gaa | 768  |
| Ala Ile Lys Ala Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu |      |
| 245 250 255   |      |
| ggc gaa gac atc agt gaa ggg aaa att gtc gat att ttc acc gca ctt | 816  |
| Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu |      |
| 260 265 270   |      |
| gaa agc caa atc gta cgt agc cgt atc att gct ggt gaa cca cgt att | 864  |
| Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile |      |
| 275 280 285   |      |
| gat ggt cgt aca gtg gat act gtt cgt gca tta gat att tgt act ggt | 912  |
| Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly |      |
| 290 295 300   |      |
| gtt tta cca cgt aca cac ggt tct gcg att ttc acc cgt ggt gaa aca | 960  |
| Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr |      |
| 305 310 315 320   |      |
| cag gcg tta gct gtc gcg aca tta ggt aca gaa cgt gat gca caa att | 1008 |
| Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile |      |
| 325 330 335   |      |
| att gat gaa tta aca ggt gag cgt tca gat cac ttc tta ttc cac tac | 1056 |
| Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr |      |
| 340 345 350   |      |
| aac ttc ccg cca tat tct gtg ggt gaa acc ggt atg att ggt tca cca | 1104 |
| Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro |      |
| 355 360 365   |      |
| aaa cgt cgt gaa att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct | 1152 |
| Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala |      |
| 370 375 380   |      |
| gca gtg atg cca aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc | 1200 |
| Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val |      |
| 385 390 395 400   |      |
| tct gaa atc aca gaa tca aat ggt tct tct tct atg gca tcg gtt tgt | 1248 |
| Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys |      |
| 405 410 415   |      |
| ggg gcg tct tta gca tta atg gat gcg ggt gta cca att aaa gcg gcg | 1296 |
| Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala |      |
| 420 425 430   |      |
| gtt gca ggt att gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg | 1344 |
| Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val |      |
| 435 440 445   |      |
| gtg ctt tca gac atc tta ggt gat gaa gat cac tta ggt gac atg gac | 1392 |
| Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp |      |
| 450 455 460   |      |
| ttc aaa gtc gcg ggt aca cgt acg ggt gtg acg gca tta caa atg gat | 1440 |
| Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp |      |
| 465 470 475 480   |      |

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atc aaa atc gaa ggt atc aca gca gaa atc atg caa att gcg tta aac 1488
Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn
485 490 495

caa gcg aaa agc gca cgt tta cac att tta ggt gtg atg gag caa gcg 1536
Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala
500 505 510

atc cca gcg cca cgt gcg gat att tct gat ttt gca ccg cgt att tac 1584
Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr
515 520 525

act atg aaa att gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt 1632
Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly
530 535 540

ggg gca acc att cgt gcc tta aca gaa gaa aca ggt acc tca att gat 1680
Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp
545 550 555 560

atc gat gat gat ggt acg gtg aag att gct gcg gtt gat ggc aat tca 1728
Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser
565 570 575

gca aaa gag gtg atg gcg cgt att gaa gat att act gca gaa gtt gaa 1776
Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu
580 585 590

gcg ggt gca gtg tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt 1824
Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly
595 600 605

gcc ttc gtt tct atc gta ggt aac aaa gaa ggc tta gtg cat att tct 1872
Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser
610 615 620

caa atc gcg gaa gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg 1920
Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val
625 630 635 640

ggg caa gaa gtg act gtt aaa gtg gtt gag att gat cgt caa ggt cgt 1968
Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg
645 650 655

att cgt tta acc atg aaa gaa gtt gca cca aag caa gaa cac gtt gat 2016
Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp
660 665 670

tct gtt gtc gca gac gtt gcc gca gaa gaa aac gca ta 2054
Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala
675 680

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&lt;210&gt; 109

&lt;211&gt; 684

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 109

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Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys
1 5 10 15

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Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr

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| 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Glu | Arg | Thr | Tyr | Ala | Ala | Gly | Arg | Ile | Pro | Gly | Gly | Phe | Phe | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Glu | Gly | Arg | Pro | Ser | Glu | Gly | Glu | Thr | Leu | Ile | Ala | Arg | Leu | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Arg | Pro | Ile | Arg | Pro | Leu | Phe | Pro | Glu | Gly | Phe | Tyr | Asn | Glu | Ile |
|     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |
| Gln | Ile | Val | Ala | Thr | Val | Val | Ser | Val | Asn | Pro | Gln | Ile | Cys | Pro | Asp |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Val | Ala | Met | Ile | Gly | Ala | Ser | Ala | Ala | Leu | Ser | Leu | Ser | Gly | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Pro | Phe | Asn | Gly | Pro | Ile | Gly | Ala | Ala | Arg | Val | Gly | Phe | Ile | Asp | Asp |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Gln | Phe | Val | Leu | Asn | Pro | Thr | Met | Asn | Glu | Gln | Lys | Gln | Ser | Arg | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Asp | Leu | Val | Val | Ala | Gly | Thr | Asp | Lys | Ala | Val | Leu | Met | Val | Glu | Ser |
|     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     | 160 |
| Glu | Ala | Asp | Val | Leu | Thr | Glu | Glu | Gln | Met | Leu | Ala | Ala | Val | Val | Phe |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gly | His | Gln | Gln | Gln | Gln | Val | Val | Ile | Asp | Ala | Ile | Lys | Glu | Phe | Thr |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ala | Glu | Ala | Gly | Lys | Pro | Arg | Trp | Asp | Trp | Val | Ala | Pro | Glu | Pro | Asn |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Thr | Ala | Leu | Ile | Glu | Lys | Val | Lys | Ala | Ile | Ala | Glu | Ala | Arg | Leu | Gly |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Glu | Ala | Tyr | Arg | Ile | Thr | Glu | Lys | Gln | Ala | Arg | Tyr | Glu | Gln | Ile | Asp |
|     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     | 240 |
| Ala | Ile | Lys | Ala | Asp | Val | Ile | Ala | Gln | Ile | Thr | Ala | Glu | Val | Ala | Glu |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     | 255 |     |
| Gly | Glu | Asp | Ile | Ser | Glu | Gly | Lys | Ile | Val | Asp | Ile | Phe | Thr | Ala | Leu |
|     |     | 260 |     |     |     |     | 265 |     |     |     |     |     | 270 |     |     |
| Glu | Ser | Gln | Ile | Val | Arg | Ser | Arg | Ile | Ile | Ala | Gly | Glu | Pro | Arg | Ile |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Asp | Gly | Arg | Thr | Val | Asp | Thr | Val | Arg | Ala | Leu | Asp | Ile | Cys | Thr | Gly |
|     | 290 |     |     |     |     | 295 |     |     |     |     |     | 300 |     |     |     |
| Val | Leu | Pro | Arg | Thr | His | Gly | Ser | Ala | Ile | Phe | Thr | Arg | Gly | Glu | Thr |
|     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |
| Gln | Ala | Leu | Ala | Val | Ala | Thr | Leu | Gly | Thr | Glu | Arg | Asp | Ala | Gln | Ile |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Ile | Asp | Glu | Leu | Thr | Gly | Glu | Arg | Ser | Asp | His | Phe | Leu | Phe | His | Tyr |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |     |
| Asn | Phe | Pro | Pro | Tyr | Ser | Val | Gly | Glu | Thr | Gly | Met | Ile | Gly | Ser | Pro |

|   |     |     |
|---|-----|-----|
| 355   | 360 | 365 |
| Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala |     |     |
| 370   | 375 | 380 |
| Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val |     |     |
| 385   | 390 | 395 |
| Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys |     |     |
|   | 405 | 410 |
|   |     | 415 |
| Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala |     |     |
|   | 420 | 425 |
|   |     | 430 |
| Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val |     |     |
|   | 435 | 440 |
|   |     | 445 |
| Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp |     |     |
|   | 450 | 455 |
|   |     | 460 |
| Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp |     |     |
| 465   | 470 | 475 |
|   |     | 480 |
| Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn |     |     |
|   | 485 | 490 |
|   |     | 495 |
| Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala |     |     |
|   | 500 | 505 |
|   |     | 510 |
| Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr |     |     |
|   | 515 | 520 |
|   |     | 525 |
| Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly |     |     |
|   | 530 | 535 |
|   |     | 540 |
| Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp |     |     |
| 545   | 550 | 555 |
|   |     | 560 |
| Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser |     |     |
|   | 565 | 570 |
|   |     | 575 |
| Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu |     |     |
|   | 580 | 585 |
|   |     | 590 |
| Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly |     |     |
|   | 595 | 600 |
|   |     | 605 |
| Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser |     |     |
|   | 610 | 615 |
|   |     | 620 |
| Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val |     |     |
| 625   | 630 | 635 |
|   |     | 640 |
| Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg |     |     |
|   | 645 | 650 |
|   |     | 655 |
| Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp |     |     |
|   | 660 | 665 |
|   |     | 670 |
| Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala                 |     |     |
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 att tat gat gcg tta acc tta ttg caa cac cgc ggg caa gac gcc gcc 96  
 Ile Tyr Asp Ala Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala  
 20 25 30  
 ggg att gta acc gta gat gat gaa aac cga ttc cgc ttg cgt aaa gcg 144  
 Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala  
 35 40 45  
 aac ggg tta gtc agc gat gta ttt gaa caa gtt cat atg tta cgt tta 192  
 Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu  
 50 55 60  
 caa ggc aat gct ggc att gga cat gtt cgt tat cct acg gct ggg agc 240  
 Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser  
 65 70 75 80  
 tca agt gtc tct gaa gcg caa cct ttt tat gta aat tcg cct tat ggc 288  
 Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly  
 85 90 95  
 tta acc tta gtg cat aat ggt aac ttg acc aat tca agt gaa tta aaa 336  
 Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys  
 100 105 110  
 gaa aag tta ttt cgt ctc gca cgt cgc cat gta aat acc aat tca gat 384  
 Glu Lys Leu Phe Arg Leu Ala Arg His Val Asn Thr Asn Ser Asp  
 115 120 125  
 tct gaa tta tta ctc aat atc tta gcc aat cac ctt gat cac ttc gaa 432  
 Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu  
 130 135 140  
 aaa tac caa tta gat ccg caa gat gta ttc agt gct gtc aaa caa acg 480  
 Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr  
 145 150 155 160  
 cat cag gat att cgt ggt gct tat gct tgt atc gcc atg att att ggt 528  
 His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly  
 165 170 175  
 cat ggt atg gtc gcg ttt cgt gat ccg aac ggt atc cgt ccg tta gtg 576  
 His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val  
 180 185 190  
 tta ggg aaa cgc gag gaa aat ggc aaa aca gag tat atg ttt gcc tcc 624  
 Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser

| 195   | 200   | 205   |      |
|---|---|---|------|
| gaa agt atc gca tta gat<br>Glu Ser Ile Ala Leu Asp<br>210   | aca gtg ggt ttt gag<br>Thr Val Gly Phe Glu<br>215 | ttt gta cga gat gta<br>Phe Val Arg Asp Val<br>220 | 672  |
| caa ccc ggc gaa gcg att tat gtc acg ttt gaa ggg gaa atg tat gct<br>Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala<br>225 230 235 240 |   |   | 720  |
| cag caa tgc gca gac aaa cca aca tta aca cct tgt att ttt gaa tac<br>Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr<br>245 250 255     |   |   | 768  |
| gtc tat ttt gca cgt cca gac tct tgc atc gat ggg gtt tct gtt tat<br>Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr<br>260 265 270     |   |   | 816  |
| gct gcc cgt gtt cat atg gga caa cgt tta ggt gaa aaa att gca cgg<br>Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg<br>275 280 285     |   |   | 864  |
| gaa tgg gcg gat gtg gat gat att gat gtg gtc att cct gtg cct gaa<br>Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu<br>290 295 300     |   |   | 912  |
| acc tct aac gat att gct tta cgt att gcg cgc gtg tta aat aaa ccg<br>Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro<br>305 310 315 320 |   |   | 960  |
| tat cgt caa ggt ttt gtg aaa aat cgc tat gta gga cgt acg ttt att<br>Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile<br>325 330 335     |   |   | 1008 |
| atg ccg ggg cag gca ttg cga gtc agt tct gtt aga cgt aaa ctc aat<br>Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn<br>340 345 350     |   |   | 1056 |
| acc att gct tca gaa ttt aaa gat aag aat gtg tta tta gtt gac gac<br>Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp<br>355 360 365     |   |   | 1104 |
| tcg att gta cgt ggt acc acg tct gaa caa att gtc gaa atg gcg aga<br>Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg<br>370 375 380     |   |   | 1152 |
| gcg gca ggt gcg aag aaa att tat ttt gcc tct gct gca cca gaa att<br>Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile<br>385 390 395 400 |   |   | 1200 |
| cgt tat cca aat gtg tat ggt att gat atg cca acc aaa aat gaa ttg<br>Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu<br>405 410 415     |   |   | 1248 |
| atc gct tat ggt cgt gat gta gat gaa att gct aac tta att ggt gtg<br>Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val<br>420 425 430     |   |   | 1296 |
| gat aaa ttg att ttc caa gat ttg gat gcg tta act ggt tct gtg caa<br>Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln<br>435 440 445     |   |   | 1344 |
| caa gaa aat cca agt att caa gac ttt gat tgt tcg gtg ttt aca ggg   |   |   | 1392 |

Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly  
 450 455 460  
 gtt tat gtg acg ggc gat att aca cct gaa tat ctg gat aat att gca 1440  
 Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala  
 465 470 475 480  
 gaa cag cgt aat gat atc gcc aag aaa aag cgt gaa aaa gat gct acc 1488  
 Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr  
 485 490 495  
 aat ctt gaa atg cac aat gaa aaa ta 1514  
 Asn Leu Glu Met His Asn Glu Lys  
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<210> 111  
 <211> 504  
 <212> PRT  
 <213> Pasteurella multocida

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 Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala  
 35 40 45  
 Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu  
 50 55 60  
 Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser  
 65 70 75 80  
 Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly  
 85 90 95  
 Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys  
 100 105 110  
 Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp  
 115 120 125  
 Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu  
 130 135 140  
 Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr  
 145 150 155 160  
 His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly  
 165 170 175  
 His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val  
 180 185 190  
 Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser  
 195 200 205  
 Glu Ser Ile Ala Leu Asp Thr Val Gly Phe Glu Phe Val Arg Asp Val  
 210 215 220



Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala  
 225 230 235 240  
 Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr  
 245 250 255  
 Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr  
 260 265 270  
 Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg  
 275 280 285  
 Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu  
 290 295 300  
 Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro  
 305 310 315 320  
 Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile  
 325 330 335  
 Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn  
 340 345 350  
 Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp  
 355 360 365  
 Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg  
 370 375 380  
 Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile  
 385 390 395 400  
 Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu  
 405 410 415  
 Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val  
 420 425 430  
 Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln  
 435 440 445  
 Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly  
 450 455 460  
 Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala  
 465 470 475 480  
 Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr  
 485 490 495  
 Asn Leu Glu Met His Asn Glu Lys  
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&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(987)

&lt;400&gt; 112

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| Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser |     |
| 1 5 10 15   |     |
| aaa aac gga gta agg aaa tca gca aca ttt aag act aaa tca gaa gct | 96  |
| Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala |     |
| 20 25 30  |     |
| aat gcg tgg gct gtt gac gag gag aga aaa tta gct gat ttg gca aaa | 144 |
| Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys |     |
| 35 40 45  |     |
| ggt atc gct cca gat att att ttt aga gat gta ata gaa cgc tat caa | 192 |
| Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln |     |
| 50 55 60  |     |
| aat gaa gtg tct ata act aaa aaa ggc gcg cga aat gaa att ata aga | 240 |
| Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg |     |
| 65 70 75 80   |     |
| tta aac cgc ttt tta aga tat gat att tct aat ctg tat att cgt gat | 288 |
| Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp |     |
| 85 90 95  |     |
| tta aga aaa gaa gat ttt gag gag tgg atc aga att cgc cta acc gaa | 336 |
| Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu |     |
| 100 105 110   |     |
| gta tcg gat gct agc gtt aga cgt gag ctt gtt act ata tcg tca gtg | 384 |
| Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val |     |
| 115 120 125   |     |
| ctg aca aca gca ata aat aag tgg gga tat att tca agg cat cca atg | 432 |
| Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met |     |
| 130 135 140   |     |
| act ggt att gaa aaa cca aaa aac tcg gca gaa aga aaa gaa cga tat | 480 |
| Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr |     |
| 145 150 155 160   |     |
| tca gaa cag gac att aaa aca ata tta gaa aca gct aga tat tgt gaa | 528 |
| Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu |     |
| 165 170 175   |     |
| gat aaa cta ccc ata aca ctc aaa caa aga gta gca att gca atg tta | 576 |
| Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu |     |
| 180 185 190   |     |
| ttt gct att gaa acc gct atg cgt gct ggt gag att gct agt ata aaa | 624 |
| Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys |     |
| 195 200 205   |     |
| tgg gat aat gtt ttt ctt gaa aag aga ata gta cat tta ccg aca act | 672 |
| Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr |     |
| 210 215 220   |     |

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aaa aac ggg cac tct aga gat gtg ccg ctt tcg caa aga gct gtt gcg 720
Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala
225                230                235                240

cta att tta aaa atg aaa gag gta gaa aat gga gat ctt gtg ttt cag 768
Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln
                245                250                255

acc acg cct gaa tca tta agc acc acg ttt aga gtg tta aag aaa gag 816
Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu
                260                265                270

tgt gga ctt gaa cat ctc cat ttt cat gat acg aga agg gaa gcg ttg 864
Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu
                275                280                285

acg aga tta tct aag aaa gta gat gta atg act cta gcc aaa att agc 912
Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser
                290                295                300

gga cat aga gat tta aga att tta caa aac aca tat tac gca ccg aat 960
Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn
305                310                315                320

atg agt gaa gtg gca aac ttg ttg gat ta 989
Met Ser Glu Val Ala Asn Leu Leu Asp
                325

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&lt;210&gt; 113

&lt;211&gt; 329

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 113

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Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser
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Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala
                20              25              30

Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys
 35              40              45

Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln
 50              55              60

Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg
 65              70              75              80

Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp
                85              90              95

Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu
 100             105             110

Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val
 115             120             125

Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met
 130             135             140

Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr

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145                      150                      155                      160  
 Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu  
                                  165                      170                      175  
 Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu  
                                  180                      185                      190  
 Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys  
                                  195                      200                      205  
 Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr  
                                  210                      215                      220  
 Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala  
                                  225                      230                      235                      240  
 Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln  
                                  245                      250                      255  
 Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu  
                                  260                      265                      270  
 Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu  
                                  275                      280                      285  
 Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser  
                                  290                      295                      300  
 Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn  
                                  305                      310                      315                      320  
 Met Ser Glu Val Ala Asn Leu Leu Asp  
                                  325

<210> 114  
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 <212> DNA  
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<220>  
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 <222> (1)..(1188)

<400> 114  
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   1                                 5                                 10                                 15  
 gca att cgc aca att caa agt cta tca acc gca gtc atc ggt att gtc 96  
 Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val  
                                  20                                 25                                 30  
 tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat gaa ccc 144  
 Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro  
                                  35                                 40                                 45  
 gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga aaa caa 192  
 Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly Lys Gln

| 50  | 55 | 60 |     |
|---|----|----|-----|
| ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc aat tgc<br>Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys<br>65 70 75 80     |    |    | 240 |
| aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac gaa gaa<br>Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu<br>85 90 95        |    |    | 288 |
| aca aaa gca agt gaa atg aac acg gca att att ggc aca atc aca gaa<br>Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu<br>100 105 110     |    |    | 336 |
| gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa aac aaa<br>Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys<br>115 120 125     |    |    | 384 |
| ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac aca aaa<br>Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys<br>130 135 140     |    |    | 432 |
| gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac gca ttt<br>Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe<br>145 150 155 160 |    |    | 480 |
| gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg gtg caa<br>Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln<br>165 170 175     |    |    | 528 |
| tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg ggc gat<br>Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp<br>180 185 190     |    |    | 576 |
| ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac tat gcc<br>Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala<br>195 200 205     |    |    | 624 |
| gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa cag ggc<br>Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly<br>210 215 220     |    |    | 672 |
| tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc ggt gtc<br>Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val<br>225 230 235 240 |    |    | 720 |
| aca caa cca ctc tat ttt gac att aac gac agc tcg act gat gtg aac<br>Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn<br>245 250 255     |    |    | 768 |
| tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat ggc ttt<br>Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe<br>260 265 270     |    |    | 816 |
| cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc aag ttt<br>Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe<br>275 280 285     |    |    | 864 |
| gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att gca ggg<br>Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly<br>290 295 300     |    |    | 912 |
| gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta gtg aaa   |    |    | 960 |

Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys  
 305 310 315 320  
 gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc aca aaa 1008  
 Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys  
 325 330 335  
 ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt aac agt 1056  
 Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser  
 340 345 350  
 gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat tat cac 1104  
 Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His  
 355 360 365  
 cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att tct gat 1152  
 Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp  
 370 375 380  
 gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg ta 1190  
 Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser  
 385 390 395  
  
 <210> 115  
 <211> 396  
 <212> PRT  
 <213> Pasteurella multocida  
  
 <400> 115  
 Met Ser Glu Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln  
 1 5 10 15  
 Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val  
 20 25 30  
 Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro  
 35 40 45  
 Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly Lys Gln  
 50 55 60  
 Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys  
 65 70 75 80  
 Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu  
 85 90 95  
 Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu  
 100 105 110  
 Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys  
 115 120 125  
 Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys  
 130 135 140  
  
 Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe  
 145 150 155 160  
 Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln  
 165 170 175

Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp  
 180 185 190  
 Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala  
 195 200 205  
 Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly  
 210 215 220  
 Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val  
 225 230 235 240  
 Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn  
 245 250 255  
 Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe  
 260 265 270  
 Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe  
 275 280 285  
 Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly  
 290 295 300  
 Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys  
 305 310 315 320  
 Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys  
 325 330 335  
 Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser  
 340 345 350  
 Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His  
 355 360 365  
 Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp  
 370 375 380  
 Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser  
 385 390 395

&lt;210&gt; 116

&lt;211&gt; 2204

&lt;212&gt; DNA

&lt;213&gt; Pasteurella multocida

&lt;220&gt;

&lt;223&gt; unkK

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2202)

&lt;400&gt; 116

atg aat aaa aat cgc tat aaa ctc att ttt agt aaa act aaa ggc tgt 48  
 Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys  
 1 5 10 15  
 ctt gta cct gtt gct gaa acg att aat tct gca gta gga aat gcc tca 96  
 Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser  
 20 25 30

|   |     |
|---|-----|
| tca aaa gac gtt tct gac acc gag ata agt gct tct caa cca gcg ctc | 144 |
| Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu |     |
| 35 40 45  |     |
| aac tcg ccg ctt tcg acc ctt tct gta tta gtc aaa acc gca ttt aat | 192 |
| Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn |     |
| 50 55 60  |     |
| ccg gtt tca aca ttg atg tcg ttg act tgg aaa gaa tac gcc gtt tta | 240 |
| Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu |     |
| 65 70 75 80   |     |
| tta tta agt gtg gtg tct ttt cct ctt atg gca caa gcc tct gat aca | 288 |
| Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr |     |
| 85 90 95  |     |
| gat tca gtg gta caa aga aaa cct gaa tta act gat gtg acg aat agc | 336 |
| Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser |     |
| 100 105 110   |     |
| aac agc tat cat gtg gaa tta gat aga gag cat cat aaa ggg gag cat | 384 |
| Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His |     |
| 115 120 125   |     |
| caa aca aaa atc aaa cat act gag aat aat gtc atc att gtt gat att | 432 |
| Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile |     |
| 130 135 140   |     |
| gca aaa cca aac caa aag ggc att tca gat aac cgt ttt aaa cac ttc | 480 |
| Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe |     |
| 145 150 155 160   |     |
| aac atc cca aat ggg gcg gta ttt aac aat agc gcc aag gaa aaa cgc | 528 |
| Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg |     |
| 165 170 175   |     |
| tca cag tta gtg ggg tat ttg cca ggt aac cag aat tta acg gaa ggt | 576 |
| Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly |     |
| 180 185 190   |     |
| agt gaa gca aaa gcg atc tta aat cag gtg act gga ccg gat gcc agt | 624 |
| Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser |     |
| 195 200 205   |     |
| aaa att gaa ggc gcc ctt gaa att tta ggg caa aaa gcc gat ttg gtg | 672 |
| Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val |     |
| 210 215 220   |     |
| att gcg aac caa aat ggc att gtg ctt aat ggg gta aaa acc att aat | 720 |
| Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn |     |
| 225 230 235 240   |     |
| gcc aat cgt ttt gtg gca aca acc agt agt acc att gat cct gag caa | 768 |
| Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln |     |
| 245 250 255   |     |
| atg cag tta aat gtc acg caa ggt aca gtg aca att ggg gtg gat gga | 816 |
| Met Gln Leu Asn Val Thr Gln Gly Thr Val Thr Ile Gly Val Asp Gly |     |
| 260 265 270   |     |
| ttt gcc aca gat ggc tta cct tat ttg gat atc att gcc aaa aag att | 864 |
| Phe Ala Thr Asp Gly Leu Pro Tyr Leu Asp Ile Ile Ala Lys Lys Ile |     |
| 275 280 285   |     |



|   |      |
|---|------|
| gaa caa aaa caa gcg att aca aaa gaa aga aca gga aat tcc gaa acc | 912  |
| Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr |      |
| 290 295 300   |      |
| gat atc act ttt gtc gca ggt aac agt aaa tat gat tta aag aca cat | 960  |
| Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His |      |
| 305 310 315 320   |      |
| caa gtg aca gaa aag cat acc gct gag gca caa ggt gaa att gcg att | 1008 |
| Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile |      |
| 325 330 335   |      |
| agc ggt gcg agt acc ggt gca atg tac ggt aaa aat atc aaa tta atc | 1056 |
| Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile |      |
| 340 345 350   |      |
| gta acg gat aaa ggc gct ggg gta aaa cat gat ggc att att tta tct | 1104 |
| Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser |      |
| 355 360 365   |      |
| gag gcg gat att caa att gaa acc cat gag ggc gat gtt gaa tta ggc | 1152 |
| Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly |      |
| 370 375 380   |      |
| aat aca aaa aat aat cag aat gag aat tat gcc aaa gct cat gcg gaa | 1200 |
| Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu |      |
| 385 390 395 400   |      |
| ggg aat ttt acg gtt aaa ggc ggt aag cac gtt att att ggt aag gaa | 1248 |
| Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu |      |
| 405 410 415   |      |
| gtt aaa gcc aac aaa gcg gtc gat att caa gca caa gaa aca aca gta | 1296 |
| Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val |      |
| 420 425 430   |      |
| aga caa aat gcg aaa tta act gcc aaa acg agt gcc aaa att aca gca | 1344 |
| Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala |      |
| 435 440 445   |      |
| agt aag agt gtg aat ctt gaa gat aac gcg aaa ctt att gct aat gag | 1392 |
| Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu |      |
| 450 455 460   |      |
| ctg agc aca aca acc aat aaa tta acc aat aaa ggt agc att tac ggc | 1440 |
| Leu Ser Thr Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly |      |
| 465 470 475 480   |      |
| aag aaa gtg acg cta gat gct gat aat tta gtc aat agt aaa gaa atc | 1488 |
| Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile |      |
| 485 490 495   |      |
| tat gcg tct agc gaa ctt gat att caa acc aaa ggt cgt gat ctt tta | 1536 |
| Tyr Ala Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu     |      |
| 500 505 510   |      |
| ctt gag gat ggg gtt aat caa cca ctg agt ttc tta aaa ggc gct tca | 1584 |
| Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser |      |
| 515 520 525   |      |
| ttg tta gcg ccg ggg ttt gtc aac act ggg cta att cac agt aac ggt | 1632 |
| Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly |      |
| 530 535 540   |      |

aat gcc aag ctc act ttt aaa gat gac acc agt ttt gtg act gaa gga 1680  
 Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly  
 545 550 555 560

aat aac ttt atc aca gca aaa gac aac tta gaa atc acg gca aaa aat 1728  
 Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn  
 565 570 575

gtt caa att gat caa gcg aaa aat att caa tta aac gcg aat atc acg 1776  
 Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr  
 580 585 590

atc aat acc aag tct ggt ttt gtg aat tac ggt acc tta gca agt gct 1824  
 Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala  
 595 600 605

caa aat tta acg att aat acc gaa caa ggc agc att tat aac ata ggc 1872  
 Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly  
 610 615 620

ggt atc ttg ggg gcg ggt aaa agt ttg aat ctg agc gcg aaa aga gga 1920  
 Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly  
 625 630 635 640

gaa aac caa gga gga tat ctt att aat caa ggt aag agt cta ctc cat 1968  
 Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His  
 645 650 655

tct gaa ggc gcc atg aac ctc aca gcg gat cgc acg gtg tac aat tta 2016  
 Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu  
 660 665 670

ggg aat att ttt gct aaa ggt gac gcg acg atc aat gca aac gcg tta 2064  
 Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu  
 675 680 685

att aat gat gtt act ctc aca ggt cgt ctt gag tat caa gat ctg aaa 2112  
 Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys  
 690 695 700

aaa gat tat acg cgt tat tat cgt atc aat gaa acg gca aaa cat ggt 2160  
 Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly  
 705 710 715 720

tgg cat aat aac ttc tat gaa tta aac gtc gac aga gtt tct tg 2204  
 Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser  
 725 730

&lt;210&gt; 117

&lt;211&gt; 734

&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 117

Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys  
 1 5 10 15

Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser  
 20 25 30

Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu  
 35 40 45

Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn  
 50 55 60  
 Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu  
 65 70 75 80  
 Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr  
 85 90 95  
 Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser  
 100 105 110  
 Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His  
 115 120 125  
 Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile  
 130 135 140  
 Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe  
 145 150 155 160  
 Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg  
 165 170 175  
 Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly  
 180 185 190  
 Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser  
 195 200 205  
 Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val  
 210 215 220  
 Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn  
 225 230 235 240  
 Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln  
 245 250 255  
 Met Gln Leu Asn Val Thr Gln Gly Thr Val Thr Ile Gly Val Asp Gly  
 260 265 270  
 Phe Ala Thr Asp Gly Leu Pro Tyr Leu Asp Ile Ile Ala Lys Lys Ile  
 275 280 285  
 Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr  
 290 295 300  
 Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His  
 305 310 315 320  
 Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile  
 325 330 335  
 Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile  
 340 345 350  
 Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser  
 355 360 365  
 Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly  
 370 375 380

Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu  
 385 390 395 400  
 Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu  
 405 410 415  
 Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val  
 420 425 430  
 Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala  
 435 440 445  
 Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu  
 450 455 460  
 Leu Ser Thr Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly  
 465 470 475 480  
 Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile  
 485 490 495  
 Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu  
 500 505 510  
 Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser  
 515 520 525  
 Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly  
 530 535 540  
 Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly  
 545 550 555 560  
 Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn  
 565 570 575  
 Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr  
 580 585 590  
 Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala  
 595 600 605  
 Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly  
 610 615 620  
 Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly  
 625 630 635 640  
 Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His  
 645 650 655  
 Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu  
 660 665 670  
 Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu  
 675 680 685  
 Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys  
 690 695 700  
 Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly  
 705 710 715 720

Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser  
 725 730

<210> 118  
 <211> 251  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <223> unkO

<220>  
 <221> CDS  
 <222> (1) .. (249)

<400> 118  
 atg aaa att act att aca cga aat cat cca gaa gta ttt caa gaa tcc 48  
 Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser  
 1 5 10 15  
 gct cgt tta gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca 96  
 Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala  
 20 25 30  
 tta aca ttg gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt 144  
 Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly  
 35 40 45  
 gag gag gaa agc aaa agg gga cat agt att aag gtt gta tta aaa gga 192  
 Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly  
 50 55 60  
 agt cac gaa gtt att aag tca gag gtg aat aca aat gaa aaa aat cat 240  
 Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His  
 65 70 75 80  
 tgt aat cat ta 251  
 Cys Asn His

<210> 119  
 <211> 83  
 <212> PRT  
 <213> Pasteurella multocida

<400> 119  
 Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser  
 1 5 10 15  
 Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala  
 20 25 30  
 Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly  
 35 40 45  
 Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly  
 50 55 60  
 Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His  
 65 70 75 80

Cys Asn His

&lt;210&gt; 120

&lt;211&gt; 548

&lt;212&gt; DNA

&lt;213&gt; Pasteurella multocida

&lt;220&gt;

&lt;223&gt; unkP

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (546)

&lt;400&gt; 120

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | cgt | gca | tat | ctt | gat | aaa | gaa | cag | ggc | tgg | cat | acg | tct | att | tca | 48  |
| Met | Arg | Ala | Tyr | Leu | Asp | Lys | Glu | Gln | Gly | Trp | His | Thr | Ser | Ile | Ser |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| aat | aaa | ggc | att | aat | ggc | gtg | agc | ggt | gtc | aca | caa | cca | ctc | tat | ttt | 96  |
| Asn | Lys | Gly | Ile | Asn | Gly | Val | Ser | Gly | Val | Thr | Gln | Pro | Leu | Tyr | Phe |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| gac | att | aac | gac | agc | tcg | act | gat | gtg | aac | tat | ctc | aat | gaa | caa | ggc | 144 |
| Asp | Ile | Asn | Asp | Ser | Ser | Thr | Asp | Val | Asn | Tyr | Leu | Asn | Glu | Gln | Gly |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| atc | acg | tgt | tgc | gtg | aat | cat | aat | ggc | ttt | cgt | ttt | tgg | ggc | tta | cgc | 192 |
| Ile | Thr | Cys | Cys | Val | Asn | His | Asn | Gly | Phe | Arg | Phe | Trp | Gly | Leu | Arg |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| acg | act | gca | gaa | gat | cca | tta | ttc | aag | ttt | gaa | gtg | tac | acc | cgc | act | 240 |
| Thr | Thr | Ala | Glu | Asp | Pro | Leu | Phe | Lys | Phe | Glu | Val | Tyr | Thr | Arg | Thr |     |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| gca | caa | atc | tta | aaa | gat | acg | att | gca | ggg | gcg | ttt | gat | tgg | gca | gtg | 288 |
| Ala | Gln | Ile | Leu | Lys | Asp | Thr | Ile | Ala | Gly | Ala | Phe | Asp | Trp | Ala | Val |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| gat | aaa | gat | att | tct | gtc | acg | cta | gtg | aaa | gat | att | att | gaa | gca | atc | 336 |
| Asp | Lys | Asp | Ile | Ser | Val | Thr | Leu | Val | Lys | Asp | Ile | Ile | Glu | Ala | Ile |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| aat | gcg | aag | tgg | cgt | gat | tac | acc | aca | aaa | ggc | tac | tta | att | ggc | ggt | 384 |
| Asn | Ala | Lys | Trp | Arg | Asp | Tyr | Thr | Thr | Lys | Gly | Tyr | Leu | Ile | Gly | Gly |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| aaa | gcg | tgg | ctt | aat | aaa | gag | ctt | aac | agt | gca | acg | aat | tta | aaa | gat | 432 |
| Lys | Ala | Trp | Leu | Asn | Lys | Glu | Leu | Asn | Ser | Ala | Thr | Asn | Leu | Lys | Asp |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| gcg | aag | ttg | ttg | atc | tct | tat | gat | tat | cac | cca | gta | cca | ccg | ctc | gaa | 480 |
| Ala | Lys | Leu | Leu | Ile | Ser | Tyr | Asp | Tyr | His | Pro | Val | Pro | Pro | Leu | Glu |     |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| cag | cta | ggc | ttt | aat | cag | tac | att | tct | gat | gaa | tac | ctt | gtt | gat | ttt | 528 |
| Gln | Leu | Gly | Phe | Asn | Gln | Tyr | Ile | Ser | Asp | Glu | Tyr | Leu | Val | Asp | Phe |     |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| tca | aat | cgt | tta | gca | tcg | ta  |     |     |     |     |     |     |     |     |     | 548 |

Ser Asn Arg Leu Ala Ser  
180

<210> 121

<211> 182

<212> PRT

<213> Pasteurella multocida

<400> 121

Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser  
1 5 10 15

Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe  
20 25 30

Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly  
35 40 45

Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg  
50 55 60

Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr  
65 70 75 80

Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val  
85 90 95

Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile  
100 105 110

Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly  
115 120 125

Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp  
130 135 140

Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu  
145 150 155 160

Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe  
165 170 175

Ser Asn Arg Leu Ala Ser  
180

<210> 122

<211> 69

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> apvA-or1

<220>

<221> CDS

<222> (1)..(69)

<400> 122

atg ttt tat gtc atg ctt gcc aat agg acg tct ata att tca tca atc 48  
Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile  
1 5 10 15

gat aag ttt aag ata ctt agc  
 Asp Lys Phe Lys Ile Leu Ser  
 20

69

<210> 123  
 <211> 23  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 123  
 Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile  
 1 5 10 15

Asp Lys Phe Lys Ile Leu Ser  
 20

<210> 124  
 <211> 64  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> apvA-or2

<220>  
 <221> CDS  
 <222> (3)..(62)

<400> 124  
 ag cta agt atc tta aac tta tcg att gat gaa att ata gac gtc cta 47  
 Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu  
 1 5 10 15

ttg gca agc atg aca ta 64  
 Leu Ala Ser Met Thr  
 20

<210> 125  
 <211> 20  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 125  
 Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu Leu  
 1 5 10 15

Ala Ser Met Thr  
 20

<210> 126  
 <211> 653  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> apvB

<220>  
 <221> CDS



&lt;222&gt; (1)..(651)

&lt;400&gt; 126

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tta att agc ttt cct ttt att act ttt gca agt aat gtt aat gga gcc 48
Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala
 1             5             10             15

gaa att gga ttg gga gga gcc cgt gag agt agt att tac tat tct aaa 96
Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys
             20             25             30

cat aaa gta gca aca aat ccc ttt tta gca ctt gat ctt tct tta ggt 144
His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly
             35             40             45

aat ttt tat atg aga ggg act gca gga att agc gaa ata gga tat gaa 192
Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu
             50             55             60

caa tct ttc act gac aat ttc agc gta tca ctg ttt gtt aac cca ttt 240
Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe
             65             70             75             80

gat ggt ttt tca att aaa gga aaa gac ttg tta cct gga tat caa agt 288
Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser
             85             90             95

att caa act cgc aaa act caa ttt gcc ttt ggt tgg gga tta aat tat 336
Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr
             100             105             110

aat ttg gga ggt tta ttc ggc tta aat gat act ttt ata tcc ttg gaa 384
Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu
             115             120             125

gga aaa agc gga aaa cgt ggt gcg agt agt aat gtc agc tta ctt aaa 432
Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys
             130             135             140

tcg ttt aat atg acg aaa aat tgg aaa gtt tca cca tat att ggc tca 480
Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser
             145             150             155             160

agt tat tat tca tct aaa tat aca gat tat tac ttt ggt att aaa caa 528
Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln
             165             170             175

tcc gaa tta ggt aat aaa att aca tcc gta tat aaa cct aaa gca gct 576
Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala
             180             185             190

tat gca aca cac ata ggt att aat act gat tat gct ttc acg aac aat 624
Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn
             195             200             205

ctt ggc atg ggt tta tct gtc ggt tgg at 653
Leu Gly Met Gly Leu Ser Val Gly Trp
             210             215

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&lt;210&gt; 127

&lt;211&gt; 217

&lt;212&gt; PRT

<213> Actinobacillus pleuropneumoniae

<400> 127

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Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala
 1           5           10           15
Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys
      20           25           30
His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly
      35           40           45
Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu
      50           55           60
Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe
      65           70           75           80
Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser
      85           90           95
Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr
      100          105          110
Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu
      115          120          125
Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys
      130          135          140
Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser
      145          150          155          160
Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln
      165          170          175
Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala
      180          185          190
Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn
      195          200          205
Leu Gly Met Gly Leu Ser Val Gly Trp
      210          215

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<210> 128

<211> 242

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> apvC

<220>

<221> CDS

<222> (1)..(240)

<400> 128

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atg tgg cgg atg gga gat ttt atg tct aaa aaa gag agg ctg aat gat   48
Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
 1           5           10           15

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```

atg gct cgc cag att tta tca gcg gcg gag ttg ctc att gca aag gaa 96
Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu
      20              25              30

ggt ttg caa aat tta tcg atg agg aaa atc gca agt gaa gcc ggt atc 144
Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
      35              40              45

gca aca ggc acg ctt tat ctc tat ttc aaa acg aaa gac gag tta ctg 192
Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
      50              55              60

gat tgt ttg gcg gaa caa tta cat gaa cga tat tat cgt tat ctg aat 240
Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
      65              70              75              80

at 242

```

<210> 129  
 <211> 80  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

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<400> 129
Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
 1              5              10              15

Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu
      20              25              30

Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
      35              40              45

Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
      50              55              60

Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
      65              70              75              80

```

<210> 130  
 <211> 527  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> apvD

<220>  
 <221> CDS  
 <222> (1)..(525)

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<400> 130
aat att caa aaa aca gtt att gct agc ggc aca ttg caa gcg act gaa 48
Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu
 1              5              10              15

caa gta gat att ggt gca caa gta tct ggg cag att aag cat att tta 96
Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
      20              25              30

gta caa gaa gga cag aag gtt aaa aaa ggt gag cta tta gct gta att 144

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```

Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile
      35              40              45

gat cca cgt ctg gct gaa acg gaa tta aaa cta gca aaa gct gag cta 192
Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu
      50              55              60

gca aat gct tct gct aat ttg gat aca aaa aaa att aat ctt aag caa 240
Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln
      65              70              75              80

ctg caa tca gat tgg gaa cgt cat caa cgt ttg ata cga acc aat gcg 288
Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala
      85              90              95

aca agc caa aag gaa aca gaa gaa gca aaa agt aga tta aat acg gcc 336
Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala
      100              105              110

aaa gca gaa ctt caa att gcg caa aat aat cta gat atc gct aaa atc 384
Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
      115              120              125

aga gtg gaa aaa gct gaa acc gaa cta gga tat aca gaa att cgt tct 432
Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
      130              135              140

cca ctt gat gca aca gta att tca gta ttt gcg caa aat ggt caa act 480
Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
      145              150              155              160

tta gtc acc acc caa caa gta cca gtg ctg atg aaa tta gct aat at 527
Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
      165              170              175

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&lt;210&gt; 131

&lt;211&gt; 175

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 131

```

Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu
  1              5              10              15

Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
      20              25              30

Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile
      35              40              45

Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu
      50              55              60

Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln
      65              70              75              80

Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala
      85              90              95

Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala
      100              105              110

```

Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile  
           115                          120                          125  
 Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser  
           130                          135                          140  
 Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr  
           145                          150                          155                          160  
 Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn  
                           165                          170                          175

<210> 132  
 <211> 867  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> atpG

<220>  
 <221> CDS  
 <222> (1)..(864)

<400> 132  
 atg gca ggt gcg aaa gag ata aga acc aaa att gca agt gtg aaa aat 48  
 Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn  
   1                          5                          10                          15  
 act caa aaa atc acc aaa gca atg gaa atg gtt gct acc tct aaa atg 96  
 Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met  
           20                          25                          30  
 cgt aaa acg caa gag cgt atg gct gcc agt cgt cct tat tcg gaa aca 144  
 Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr  
           35                          40                          45  
 atc cgt aag gtg att agc cat att gcg aaa gga agc att ggt tat aag 192  
 Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys  
           50                          55                          60  
 cac ccg ttt tta act gaa cgt gat att aaa aaa gta ggc tat ctt gtc 240  
 His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val  
           65                          70                          75                          80  
 gtt tcg acc gat cgc ggt tta tgc ggt ggc ctt aat atc aat tta ttc 288  
 Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe  
           85                          90                          95  
 aaa gcg act ttg aat gaa ttt aaa acg tgg aaa gat aaa gac gtt agt 336  
 Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser  
           100                          105                          110  
 gtt gag ctt ggt tta gta ggg tcg aaa ggc gta agc ttt tac caa aat 384  
 Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn  
           115                          120                          125  
 cta ggc tta aac gtg aga tct caa gta acg gga tta ggc gat aat ccg 432  
 Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro  
           130                          135                          140  
 gaa atg gaa cgt atc gtg ggc gca gtt aat gaa atg att aat gcg ttc 480

Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe  
 145 150 155 160  
 cga aac gga gaa gtg gat gcg gtt tac gtc gct tac aac cgt ttt gaa 528  
 Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu  
 165 170 175  
 aat acg atg tca caa aaa cct gtt atc gca cag tta ctt ccg tta cct 576  
 Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro  
 180 185 190  
 aaa cta gat gac gat gaa tta gat acg aaa ggt tca tgg gat tat att 624  
 Lys Leu Asp Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile  
 195 200 205  
 tat gaa ccg aat cca caa gtt tta ttg gat agt tta ctt gtt cgt tat 672  
 Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr  
 210 215 220  
 tta gaa act cag gta tac caa gca gtt gta gat aac cta gct tct gaa 720  
 Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu  
 225 230 235 240  
 caa gcc gct cga atg gta gcg atg aaa gcc gca aca gat aat gcg ggt 768  
 Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly  
 245 250 255  
 aca tta atc gat gaa tta caa tta gtg tat aac aaa gct cgc caa gca 816  
 Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala  
 260 265 270  
 agc att aca aat gaa tta aac gaa att gtt gcg ggt gcc gca gca att 864  
 Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile  
 275 280 285  
 taa 867  
  
 <210> 133  
 <211> 288  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae  
  
 <400> 133  
 Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn  
 1 5 10 15  
 Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met  
 20 25 30  
 Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr  
 35 40 45  
  
 Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys  
 50 55 60  
 His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val  
 65 70 75 80  
 Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe  
 85 90 95

Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser  
                   100                                  105                                  110  
 Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn  
                   115                                  120                                  125  
 Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro  
                   130                                  135                                  140  
 Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe  
                   145                                  150                                  155                                  160  
 Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu  
                                   165                                  170                                  175  
 Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro  
                                   180                                  185                                  190  
 Lys Leu Asp Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile  
                   195                                  200                                  205  
 Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr  
                   210                                  215                                  220  
 Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu  
                   225                                  230                                  235                                  240  
 Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly  
                                   245                                  250                                  255  
 Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala  
                                   260                                  265                                  270  
 Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile  
                   275                                  280                                  285

<210> 134  
 <211> 534  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> atpH

<220>  
 <221> CDS  
 <222> (1)..(531)

<400> 134  
 atg tca gaa tta agt aca gta gct cgc ccc tac gct aaa gca gct ttt 48  
 Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe  
       1                                  5                                  10                                  15  
 gat ttt gct tta gaa caa ggt cag ttg gac aaa tgg caa gaa atg tta 96  
 Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu  
                   20                                  25                                  30  
 cag ttt tgg gca ttc gtt gct gaa aac gaa caa gtg gcg gaa tat att 144  
 Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile  
                   35                                  40                                  45  
 aat tct tcc ctt gca agc ggt cag att tct gaa act ttt atc aaa atc 192

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Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
  50                      55                      60

tgc ggc gac caa ctt gat caa tat ggg caa aat ttt att cgt gta atg   240
Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met
  65                      70                      75                      80

gct gaa aat aaa cgt ctg gct gtg ttg cct atg gtt ttt gat act ttc   288
Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe
                      85                      90                      95

gta tca tta cga gcg gaa cat gaa gcg gta aaa gat gta aca att gtt   336
Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val
                      100                      105                      110

tcg gca aac gaa tta agt caa gca caa gaa gat aaa atc gca aaa gcg   384
Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
                      115                      120                      125

atg gaa aaa cgc tta ggt caa aaa gtt cgt tta acc aac caa atc gat   432
Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp
                      130                      135                      140

aac agc ctg att gca ggc gta att att aaa tac gat gat gtt gtt att   480
Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
                      145                      150                      155                      160

gat ggt agt agc cgc ggt cag tta aat cgc tta gcg tca gcg ttg agc   528
Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
                      165                      170                      175

ttg taa
Leu

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534

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<210> 135
<211> 177
<212> PRT
<213> Actinobacillus pleuropneumoniae

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<400> 135
Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
  1                      5                      10                      15

Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu
                      20                      25                      30

Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile
                      35                      40                      45

Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
  50                      55                      60

Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met
  65                      70                      75                      80

Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe
                      85                      90                      95

Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val
                      100                      105                      110

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Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
      115                      120                      125

Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp
      130                      135                      140

Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
      145                      150                      155                      160

Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
      165                      170                      175

Leu

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<210> 136
<211> 321
<212> DNA
<213> Actinobacillus pleuropneumoniae

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<220>
<223> dksA

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<220>
<221> CDS
<222> (1)..(318)

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<400> 136
gca tgg cat gtg caa att atg gac gaa gct gag cgt aca aaa aac caa 48
Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
  1                      5                      10                      15

atg cag gaa gaa gtc gct aat ttc gcc gat cct gcg gac cgc gcc act 96
Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
      20                      25                      30

cag gaa gaa gaa ttc agt ctt gaa tta aga aac cgt gac cgt gag cgt 144
Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
      35                      40                      45

aaa ttg ctt aag aag att gag caa acg tta aat agc att gcc gaa gac 192
Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
      50                      55                      60

gaa tac ggc tat tgc gaa act tgc ggt gtt gaa atc ggt tta cgt cgt 240
Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
      65                      70                      75                      80

tta gaa gcg cgc ccg acc gcg gat atg tgt atc gat tgc aaa aca ctt 288
Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
      85                      90                      95

gcg gaa atc cgt gaa aag caa atg ggc tta taa 321
Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
      100                      105

```

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<210> 137
<211> 106
<212> PRT
<213> Actinobacillus pleuropneumoniae

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&lt;400&gt; 137

Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln  
 1 5 10 15

Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr  
 20 25 30

Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg  
 35 40 45

Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp  
 50 55 60

Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg  
 65 70 75 80

Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu  
 85 90 95

Ala Glu Ile Arg Glu Lys Gln Met Gly Leu  
 100 105

&lt;210&gt; 138

&lt;211&gt; 33

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; dnaK

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(30)

&lt;400&gt; 138

gct gag ttt gaa gaa gtg aaa gat aat aaa taa  
 Ala Glu Phe Glu Glu Val Lys Asp Asn Lys  
 1 5 10

33

&lt;210&gt; 139

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 139

Ala Glu Phe Glu Glu Val Lys Asp Asn Lys  
 1 5 10

&lt;210&gt; 140

&lt;211&gt; 453

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; exbB

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(450)

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<400> 140
atg gaa caa atg ctt gaa ctt tta caa ggt cat gtt gat tat att att 48
Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
  1             5             10             15

tta ggc tta tta cta tta atg agt gtt gtg ttg gta tgg aaa att att 96
Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
             20             25             30

gaa cgc gta ctt ttc tac aaa caa ttg gat gtg acc aaa tat gac acg 144
Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr
             35             40             45

cta caa gat ttg gaa att gat acc act cgc aat tta acc acc att tcc 192
Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser
             50             55             60

act atc ggt gcc aac gcc cct tat atc ggt tta tta gga acc gta tta 240
Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu
             65             70             75             80

ggg atc tta ctt acc ttc tat cat tta ggg cat tcc ggc ggt gat att 288
Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile
             85             90             95

gac gcc gca tcc att atg gtt cac ctt tcg ctt gca tta aaa gca acc 336
Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr
             100             105             110

gca gcc ggt atc tta gtc gct att ccg gca atg atg ttc tac agc ggt 384
Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly
             115             120             125

ttt aac cgt aaa gtg gat gaa agc aaa ctt aaa tgg caa gcg att caa 432
Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln
             130             135             140

gct cgt aaa gcc aat caa taa 453
Ala Arg Lys Ala Asn Gln
145             150

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<210> 141
<211> 150
<212> PRT
<213> Actinobacillus pleuropneumoniae

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<400> 141
Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
  1             5             10             15

Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
             20             25             30

Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr
             35             40             45

Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser
             50             55             60

Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu
             65             70             75             80

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Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile  
                                     85                                    90                                    95

Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr  
                                     100                                    105                                    110

Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly  
                                     115                                    120                                    125

Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln  
                                     130                                    135                                    140

Ala Arg Lys Ala Asn Gln  
 145                                    150

<210> 142  
 <211> 720  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> fkpA

<220>  
 <221> CDS  
 <222> (1)..(717)

<400> 142  
 atg tta aaa aat aaa ctt tct gtt ctt gca atc gta gcc ggt acg ttc 48  
 Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe  
     1                                    5                                    10                                    15

gtt tca gct caa act gca ttt gca gcg gat caa aaa ttc att gac gat 96  
 Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp  
                                     20                                    25                                    30

tca tca tat gca gtc ggc gta ttg atg ggt aaa aat atc gaa ggc gtc 144  
 Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val  
                                     35                                    40                                    45

gtt gaa tca caa aaa gaa att ttt tct tat aac caa gat aaa atc ttg 192  
 Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu  
     50                                    55                                    60

gcg ggt gtc caa gat acc atc aaa aaa acc ggt aaa tta acc gat gaa 240  
 Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu  
     65                                    70                                    75                                    80

gat cta caa aaa caa tta aaa tcg ctt gat act tat ctt gca agt caa 288  
 Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln  
                                     85                                    90                                    95

gaa agc aaa att gcg gcg gag aaa agc aaa gca acc gta gaa gcc ggt 336  
 Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly  
                                     100                                    105                                    110

aat aaa ttt cgt acc gac tac gaa aaa caa agc ggc gtg aaa aaa acc 384  
 Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr  
                                     115                                    120                                    125

gct tcc ggt tta ctt tat aaa att gaa aaa gcc ggc acg ggc gaa tcg 432

Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser  
 130 135 140

cct aaa gcg gaa gat acc gtt aaa gtt cac tat aaa ggg aca tta acc 480  
 Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr  
 145 150 155 160

gat ggt acg gta ttc gat agc tca tac gat cgc ggt gag ccg att gaa 528  
 Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu  
 165 170 175

ttc caa tta aac caa tta att ccg ggt tgg att gaa gcg att cca atg 576  
 Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met  
 180 185 190

ttg aaa aaa ggc gga aaa atg gaa atc gtc gtt ccg cct gaa ctt ggt 624  
 Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly  
 195 200 205

tac ggc gaa cgc caa gca ggt aag att ccg gca agt tca acc tta aaa 672  
 Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys  
 210 215 220

ttc gag att gaa ttg tta gat ttc aaa gcg gcc gaa gcg aaa aaa taa 720  
 Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys  
 225 230 235

&lt;210&gt; 143

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 143

Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe  
 1 5 10 15

Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp  
 20 25 30

Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val  
 35 40 45

Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu  
 50 55 60

Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu  
 65 70 75 80

Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln  
 85 90 95

Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly  
 100 105 110

Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr  
 115 120 125

Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser  
 130 135 140

Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr  
 145 150 155 160

Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu  
 165 170 175  
 Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met  
 180 185 190  
 Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly  
 195 200 205  
 Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys  
 210 215 220  
 Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys  
 225 230 235

<210> 144  
 <211> 290  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> HI0379

<220>  
 <221> CDS  
 <222> (3)..(287)

<400> 144  
 tg cat agc gtg aga ggt ccg ggc ggc ggt tat caa ctc ggt aag caa 47  
 His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln  
 1 5 10 15  
 cct gaa gag att agt gtg ggg atg att att gcg gcg gtg aat gaa aat 95  
 Pro Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn  
 20 25 30  
 ctc gac gta acc aaa tgt aaa ggt agc ggc aac tgt agc aaa aac tct 143  
 Leu Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser  
 35 40 45  
 cag tgc tta acc cat cat tta tgg gaa cgt tta gaa gaa caa atc ggt 191  
 Gln Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly  
 50 55 60  
 gtg ttt tta aat acg att act tta gcg gaa ctt gtt gaa gaa cat tcg 239  
 Val Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser  
 65 70 75  
 gat cac gat tgt gaa aaa gaa cat tgc cac gat cat tca cac aaa cat 287  
 Asp His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His  
 80 85 90 95  
 taa 290

<210> 145  
 <211> 95  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 145  
 His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln Pro

|   |   |                 |    |
|---|---|-----------------|----|
| 1   | 5   | 10              | 15 |
| Glu Glu Ile   | Ser Val Gly Met Ile Ile Ala Ala Val                 | Asn Glu Asn Leu |    |
|   | 20  | 25              | 30 |
| Asp Val Thr   | Lys Cys Lys Gly Ser Gly Asn Cys Ser                 | Lys Asn Ser Gln |    |
|   | 35  | 40              | 45 |
| Cys Leu Thr   | His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly Val |                 |    |
|   | 50  | 55              | 60 |
| Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser Asp |   |                 |    |
| 65  | 70  | 75              | 80 |
| His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His     |   |                 |    |
|   | 85  | 90              | 95 |

<210> 146  
 <211> 273  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> hupA

<220>  
 <221> CDS  
 <222> (1)..(270)

|   |     |
|---|-----|
| <400> 146   |     |
| atg aac aaa act gag tta atc gat gca atc gca gct ggt gca gag tta | 48  |
| Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu |     |
| 1 5 10 15   |     |
| agc aag aaa gac gcg aaa gcg gca tta gaa gcg act tta aat gcg atc | 96  |
| Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile |     |
| 20 25 30  |     |
| tct gaa agc cta aaa aat ggc gac acc gtt cag tta atc ggc ttc ggt | 144 |
| Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly |     |
| 35 40 45  |     |
| act ttt aaa gta aac gag cgt aat gca cgt acg ggt cgt aac ccg cgt | 192 |
| Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg |     |
| 50 55 60  |     |
| acc ggc gaa gaa atc aaa atc gca gca tct aaa gtg ccg gcg ttt gtt | 240 |
| Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val |     |
| 65 70 75 80   |     |
| gca ggt aaa gca tta aaa gat tta gta aaa taa                     | 273 |
| Ala Gly Lys Ala Leu Lys Asp Leu Val Lys                         |     |
| 85 90   |     |

<210> 147  
 <211> 90  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 147  
 Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu

|   |    |    |    |
|---|----|----|----|
| 1   | 5  | 10 | 15 |
| Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile |    |    |    |
|   | 20 | 25 | 30 |
| Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly |    |    |    |
|   | 35 | 40 | 45 |
| Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg |    |    |    |
|   | 50 | 55 | 60 |
| Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val |    |    |    |
|   | 65 | 70 | 75 |
| Ala Gly Lys Ala Leu Lys Asp Leu Val Lys                         |    |    |    |
|   | 85 | 90 |    |

&lt;210&gt; 148

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; lpdA

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(549)

&lt;400&gt; 148

|   |     |
|---|-----|
| atg agc aaa gaa atc aaa acg caa gtc gtg gta ctt ggt gcg ggt cct | 48  |
| Met Ser Lys Glu Ile Lys Thr Gln Val Val Val Leu Gly Ala Gly Pro |     |
| 1 5 10 15   |     |
| gcc ggt tat tca gcg gca ttc cgt tgt gcc gac tta ggc tta gaa aca | 96  |
| Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr |     |
| 20 25 30  |     |
| gta att gtc gaa cgt tat tca act ttg ggc ggt gta tgc tta aac gta | 144 |
| Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val |     |
| 35 40 45  |     |
| ggc tgt att ccg tct aaa gca tta tta cac gtt gca aaa gtt atc gaa | 192 |
| Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu |     |
| 50 55 60  |     |
| gaa gca aaa cac gca gag aaa aac ggt att act ttc ggt gag ccc aac | 240 |
| Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn |     |
| 65 70 75 80   |     |
| att gat tta gat aaa gtg cgt gcg ggt aaa gaa gcg gtt gtt tct aaa | 288 |
| Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys |     |
| 85 90 95  |     |
| tta acc ggc ggt tta gcg ggt atg gct aaa gca cgt aaa gta aca gta | 336 |
| Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val |     |
| 100 105 110   |     |
| gtg gaa ggt tta gcg gcg ttt acc gat ccg aat act tta gta gct cgt | 384 |
| Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg |     |
| 115 120 125   |     |



gac cgt gac ggt aat ccg aca acg att aaa ttt gat tat gca att att 432  
 Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile  
 130 135 140  
 gca gcc ggt tct cgt ccg att cag ctt ccg ttc att cca cac gaa gat 480  
 Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp  
 145 150 155 160  
 ccg cgt gtg tgg gat tct acg gat gca ctt aaa tta aaa gaa gta ccc 528  
 Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro  
 165 170 175  
 gaa aaa att act cat tat ggg cc 551  
 Glu Lys Ile Thr His Tyr Gly  
 180

&lt;210&gt; 149

&lt;211&gt; 183

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 149

Met Ser Lys Glu Ile Lys Thr Gln Val Val Val Leu Gly Ala Gly Pro  
 1 5 10 15  
 Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr  
 20 25 30  
 Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val  
 35 40 45  
 Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu  
 50 55 60  
 Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn  
 65 70 75 80  
 Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys  
 85 90 95  
 Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val  
 100 105 110  
 Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg  
 115 120 125  
 Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile  
 130 135 140  
 Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp  
 145 150 155 160  
 Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro  
 165 170 175  
 Glu Lys Ile Thr His Tyr Gly  
 180

&lt;210&gt; 150

&lt;211&gt; 1095

&lt;212&gt; DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> Omp5-2

<220>

<221> CDS

<222> (1) .. (1092)

<400> 150

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atg aaa aaa tca tta gtt gct tta aca gta tta tcg gct gca gcg gta 48
Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Ala Val
  1             5             10             15

gct caa gca gcg cca caa caa aat act ttc tac gca ggt gcg aaa gca 96
Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala
             20             25             30

ggt tgg gcg tca ttc cat gat ggt atc gaa caa tta gat tca gct aaa 144
Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys
             35             40             45

aac aca gat cgc ggt aca aaa tac ggt atc aac cgt aat tca gta act 192
Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr
             50             55             60

tac ggc gta ttc ggc ggt tac caa att tta aac caa gac aaa tta ggt 240
Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly
             65             70             75             80

tta gcg gct gaa tta ggt tat gac tat ttc ggt cgt gtg cgc ggt tct 288
Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser
             85             90             95

gaa aaa cca aac ggt aaa gcg gac aag aaa act ttc cgt cac gct gca 336
Glu Lys Pro Asn Gly Lys Ala Asp Lys Lys Thr Phe Arg His Ala Ala
             100            105            110

cac ggt gcg aca atc gca tta aaa cct agc tac gaa gta tta cct gac 384
His Gly Ala Thr Ile Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp
             115            120            125

tta gac gtt tac ggt aaa gta ggt atc gca tta gta aac aat aca tat 432
Leu Asp Val Tyr Gly Lys Val Gly Ile Ala Leu Val Asn Asn Thr Tyr
             130            135            140

aaa aca ttc aat gca gca caa gag aaa gtg aaa act cgt cgt ttc caa 480
Lys Thr Phe Asn Ala Ala Gln Glu Lys Val Lys Thr Arg Arg Phe Gln
             145            150            155            160

agt tct tta att tta ggt gcg ggt gtt gag tac gca att ctt cct gaa 528
Ser Ser Leu Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro Glu
             165            170            175

tta gcg gca cgt gtt gaa tac caa tgg tta aac aac gca ggt aaa gca 576
Leu Ala Ala Arg Val Glu Tyr Gln Trp Leu Asn Asn Ala Gly Lys Ala
             180            185            190

agc tac tct act tta aat cgt atg ggt gca act gac tac cgt tcg gat 624
Ser Tyr Ser Thr Leu Asn Arg Met Gly Ala Thr Asp Tyr Arg Ser Asp
             195            200            205

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atc agt tcc gta tct gca ggt tta agc tac cgt ttc ggt caa ggt gcg 672  
 Ile Ser Ser Val Ser Ala Gly Leu Ser Tyr Arg Phe Gly Gln Gly Ala  
 210 215 220  
 gca ccg gtt gca gct ccg gca gtt gaa act aaa aac ttc gca ttc agc 720  
 Ala Pro Val Ala Ala Pro Ala Val Glu Thr Lys Asn Phe Ala Phe Ser  
 225 230 235 240  
 tct gac gta tta ttc gca ttc ggt aaa tca aac tta aaa ccg gct gcg 768  
 Ser Asp Val Leu Phe Ala Phe Gly Lys Ser Asn Leu Lys Pro Ala Ala  
 245 250 255  
 gca aca gca tta gat gca atg caa acc gaa atc aat aac gca ggt tta 816  
 Ala Thr Ala Leu Asp Ala Met Gln Thr Glu Ile Asn Asn Ala Gly Leu  
 260 265 270  
 tca aat gct gcg atc caa gta aac ggt tac acg gac cgt atc ggt aaa 864  
 Ser Asn Ala Ala Ile Gln Val Asn Gly Tyr Thr Asp Arg Ile Gly Lys  
 275 280 285  
 gaa gct tca aac tta aaa ctt tca caa cgt cgt gcg gaa aca gta gct 912  
 Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg Ala Glu Thr Val Ala  
 290 295 300  
 aac tac atc gtt tct aaa ggt gct ccg gca gct aac gta act gca gta 960  
 Asn Tyr Ile Val Ser Lys Gly Ala Pro Ala Asn Val Thr Ala Val  
 305 310 315 320  
 ggt tac ggt gaa gca aac cct gta acc ggc gca aca tgt gac aaa gtt 1008  
 Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala Thr Cys Asp Lys Val  
 325 330 335  
 aaa ggt cgt aaa gca tta atc gct tgc tta gca ccg gat cgt cgt gtt 1056  
 Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala Pro Asp Arg Arg Val  
 340 345 350  
 gaa gtt caa gtt caa ggt act aaa gaa gta act atg taa 1095  
 Glu Val Gln Val Gln Gly Thr Lys Glu Val Thr Met  
 355 360

&lt;210&gt; 151

&lt;211&gt; 364

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 151

Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Ala Val  
 1 5 10 15  
 Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala  
 20 25 30  
 Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys  
 35 40 45  
 Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr  
 50 55 60  
 Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly  
 65 70 75 80  
 Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser

| 85  |     |     |     |     |     |     |     |     |     | 90  |     |     |     |     | 95  |  |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|
| Glu | Lys | Pro | Asn | Gly | Lys | Ala | Asp | Lys | Lys | Thr | Phe | Arg | His | Ala | Ala |  |  |  |  |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |  |  |  |  |
| His | Gly | Ala | Thr | Ile | Ala | Leu | Lys | Pro | Ser | Tyr | Glu | Val | Leu | Pro | Asp |  |  |  |  |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |  |  |  |
| Leu | Asp | Val | Tyr | Gly | Lys | Val | Gly | Ile | Ala | Leu | Val | Asn | Asn | Thr | Tyr |  |  |  |  |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |  |  |  |  |
| Lys | Thr | Phe | Asn | Ala | Ala | Gln | Glu | Lys | Val | Lys | Thr | Arg | Arg | Phe | Gln |  |  |  |  |  |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |  |  |  |
| Ser | Ser | Leu | Ile | Leu | Gly | Ala | Gly | Val | Glu | Tyr | Ala | Ile | Leu | Pro | Glu |  |  |  |  |  |  |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |  |  |  |  |  |  |
| Leu | Ala | Ala | Arg | Val | Glu | Tyr | Gln | Trp | Leu | Asn | Asn | Ala | Gly | Lys | Ala |  |  |  |  |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |  |  |  |  |
| Ser | Tyr | Ser | Thr | Leu | Asn | Arg | Met | Gly | Ala | Thr | Asp | Tyr | Arg | Ser | Asp |  |  |  |  |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |  |  |  |
| Ile | Ser | Ser | Val | Ser | Ala | Gly | Leu | Ser | Tyr | Arg | Phe | Gly | Gln | Gly | Ala |  |  |  |  |  |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |  |  |  |
| Ala | Pro | Val | Ala | Ala | Pro | Ala | Val | Glu | Thr | Lys | Asn | Phe | Ala | Phe | Ser |  |  |  |  |  |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |  |  |  |  |  |
| Ser | Asp | Val | Leu | Phe | Ala | Phe | Gly | Lys | Ser | Asn | Leu | Lys | Pro | Ala | Ala |  |  |  |  |  |  |
|     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |  |  |  |  |  |  |
| Ala | Thr | Ala | Leu | Asp | Ala | Met | Gln | Thr | Glu | Ile | Asn | Asn | Ala | Gly | Leu |  |  |  |  |  |  |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |  |  |  |  |  |
| Ser | Asn | Ala | Ala | Ile | Gln | Val | Asn | Gly | Tyr | Thr | Asp | Arg | Ile | Gly | Lys |  |  |  |  |  |  |
|     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |     |  |  |  |  |  |  |
| Glu | Ala | Ser | Asn | Leu | Lys | Leu | Ser | Gln | Arg | Arg | Ala | Glu | Thr | Val | Ala |  |  |  |  |  |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |  |  |  |  |  |
| Asn | Tyr | Ile | Val | Ser | Lys | Gly | Ala | Pro | Ala | Ala | Asn | Val | Thr | Ala | Val |  |  |  |  |  |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |  |  |  |  |  |
| Gly | Tyr | Gly | Glu | Ala | Asn | Pro | Val | Thr | Gly | Ala | Thr | Cys | Asp | Lys | Val |  |  |  |  |  |  |
|     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |     |  |  |  |  |  |  |
| Lys | Gly | Arg | Lys | Ala | Leu | Ile | Ala | Cys | Leu | Ala | Pro | Asp | Arg | Arg | Val |  |  |  |  |  |  |
|     |     | 340 |     |     |     |     | 345 |     |     |     |     |     | 350 |     |     |  |  |  |  |  |  |
| Glu | Val | Gln | Val | Gln | Gly | Thr | Lys | Glu | Val | Thr | Met |     |     |     |     |  |  |  |  |  |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     |     |     |     |     |  |  |  |  |  |  |

&lt;210&gt; 152

&lt;211&gt; 1110

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; Omp5

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1107)

&lt;400&gt; 152

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | aaa | aaa | tca | tta | gtt | gct | tta | gca | gta | tta | tcg | gct | gca | gca | gta | 48  |
| Met | Lys | Lys | Ser | Leu | Val | Ala | Leu | Ala | Val | Leu | Ser | Ala | Ala | Ala | Val |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| gct | caa | gca | gct | cca | caa | caa | aat | act | ttc | tac | gca | ggt | gcg | aaa | gtt | 96  |
| Ala | Gln | Ala | Ala | Pro | Gln | Gln | Asn | Thr | Phe | Tyr | Ala | Gly | Ala | Lys | Val |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| ggt | caa | tca | tca | ttt | cac | cac | ggt | gtt | aac | caa | tta | aaa | tct | ggt | cac | 144 |
| Gly | Gln | Ser | Ser | Phe | His | His | Gly | Val | Asn | Gln | Leu | Lys | Ser | Gly | His |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| gat | gat | cgt | tat | aat | gat | aaa | aca | cgt | aag | tat | ggt | atc | aac | cgt | aac | 192 |
| Asp | Asp | Arg | Tyr | Asn | Asp | Lys | Thr | Arg | Lys | Tyr | Gly | Ile | Asn | Arg | Asn |     |
|     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| tct | gta | act | tac | ggt | gta | ttc | ggc | ggt | tac | caa | atc | tta | aac | caa | aat | 240 |
| Ser | Val | Thr | Tyr | Gly | Val | Phe | Gly | Gly | Tyr | Gln | Ile | Leu | Asn | Gln | Asn |     |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| aac | ttc | ggt | tta | gca | gct | gaa | tta | ggc | tat | gac | tac | tac | ggt | cgc | gta | 288 |
| Asn | Phe | Gly | Leu | Ala | Ala | Glu | Leu | Gly | Tyr | Asp | Tyr | Tyr | Gly | Arg | Val |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| cgt | ggt | aac | gta | gat | gaa | ttc | cgt | aca | gtt | aaa | cac | tct | gct | cac | ggt | 336 |
| Arg | Gly | Asn | Val | Asp | Glu | Phe | Arg | Thr | Val | Lys | His | Ser | Ala | His | Gly |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| tta | aac | tta | gcg | tta | aaa | cca | agc | tac | gaa | gta | tta | cct | gac | tta | gac | 384 |
| Leu | Asn | Leu | Ala | Leu | Lys | Pro | Ser | Tyr | Glu | Val | Leu | Pro | Asp | Leu | Asp |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| gtt | tac | ggt | aaa | gta | ggt | att | gcg | gtt | gtt | cgt | aat | gac | tat | aaa | aaa | 432 |
| Val | Tyr | Gly | Lys | Val | Gly | Ile | Ala | Val | Val | Arg | Asn | Asp | Tyr | Lys | Lys |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| tat | ggt | gcg | gaa | aac | act | aac | gaa | tca | aca | aca | aaa | ttc | cac | aaa | tta | 480 |
| Tyr | Gly | Ala | Glu | Asn | Thr | Asn | Glu | Ser | Thr | Thr | Lys | Phe | His | Lys | Leu |     |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| aaa | gca | tca | act | att | tta | ggt | gca | ggt | gtt | gag | tac | gca | att | ctt | cct | 528 |
| Lys | Ala | Ser | Thr | Ile | Leu | Gly | Ala | Gly | Val | Glu | Tyr | Ala | Ile | Leu | Pro |     |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| gaa | tta | gcg | gca | cgt | gtt | gaa | tac | caa | tac | tta | aac | aaa | gcg | ggt | aac | 576 |
| Glu | Leu | Ala | Ala | Arg | Val | Glu | Tyr | Gln | Tyr | Leu | Asn | Lys | Ala | Gly | Asn |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| tta | aat | aaa | gca | tta | gtt | cgt | tca | ggc | aca | caa | gat | gtg | gac | ttc | caa | 624 |
| Leu | Asn | Lys | Ala | Leu | Val | Arg | Ser | Gly | Thr | Gln | Asp | Val | Asp | Phe | Gln |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| tat | gct | cct | gat | atc | cac | tct | gta | aca | gca | ggt | tta | tca | tac | cgt | ttc | 672 |
| Tyr | Ala | Pro | Asp | Ile | His | Ser | Val | Thr | Ala | Gly | Leu | Ser | Tyr | Arg | Phe |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| ggt | caa | ggc | gct | gta | gca | cca | gtt | gtt | gag | cca | gaa | gtt | gta | act | aaa | 720 |
| Gly | Gln | Gly | Ala | Val | Ala | Pro | Val | Val | Glu | Pro | Glu | Val | Val | Thr | Lys |     |
|     | 225 |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |

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aac ttc gca ttc agc tca gac gtt tta ttt gat ttc ggt aaa tca agc 768
Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser
245 250 255

tta aaa cca gca gca gca aca gct tta gac gca gct aac act gaa atc 816
Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile
260 265 270

gct aac tta ggt tta gca act cca gct atc caa gtt aac ggt tat aca 864
Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr
275 280 285

gac cgt atc ggt aaa gaa gct tca aac tta aaa ctt tca caa cgc cgt 912
Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg
290 295 300

gca gaa act gta gct aac tac tta gtt tct aaa ggt caa aac cct gca 960
Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala
305 310 315 320

aac gta act gca gta ggt tac ggt gaa gca aac cca gta acc ggc gca 1008
Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala
325 330 335

aca tgt gat gca gtt aaa ggt cgt aaa gca tta atc gct tgc tta gca 1056
Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala
340 345 350

ccg gat cgt cgt gtt gaa gtt caa gta caa ggt gct aaa aac gta gct 1104
Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala
355 360 365

atg taa 1110
Met

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&lt;210&gt; 153

&lt;211&gt; 369

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 153

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Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val
1 5 10 15

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val
20 25 30

Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His
35 40 45

Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn
50 55 60

Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn
65 70 75 80

Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val
85 90 95

Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly
100 105 110

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Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp  
 115 120 125  
 Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys  
 130 135 140  
 Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu  
 145 150 155 160  
 Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro  
 165 170 175  
 Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn  
 180 185 190  
 Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln  
 195 200 205  
 Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe  
 210 215 220  
 Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys  
 225 230 235 240  
 Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser  
 245 250 255  
 Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile  
 260 265 270  
 Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr  
 275 280 285  
 Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg  
 290 295 300  
 Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala  
 305 310 315 320  
 Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala  
 325 330 335  
 Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala  
 340 345 350  
 Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala  
 355 360 365

Met

&lt;210&gt; 154

&lt;211&gt; 1076

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; pnp new

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1074)

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<400> 154
aat att aaa gaa ttc gta aaa gaa gcg ggt aaa ccg cgt tgg gat tgg 48
Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp
1 5 10 15

gtt gcg ccg gaa ccg aat acc gca tta atc aac caa gtt aaa gcg tta 96
Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu
20 25 30

gcg gaa gcg cgt atc ggc gat ccg tat cgt att aca gaa aaa caa gcg 144
Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala
35 40 45

cgt tac gaa caa atc gat gca att aaa gcg gat gtt atc gca caa tta 192
Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu
50 55 60

acc gca caa gac gaa acc gtt tct gaa ggt gcg att att gat att att 240
Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile
65 70 75 80

acc gca tta gaa agt tct att gtt cgc ggt cgt att att gcc ggc gaa 288
Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu
85 90 95

ccg cgt att gac ggt cgt acg gta gat acg gtt cgt gca tta gac att 336
Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile
100 105 110

tgc acc ggc gta tta cct cgt acg cac ggt tct gca atc ttt act cgc 384
Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg
115 120 125

ggg gaa aca caa gca tta gcg gtt gca acc tta ggt act gag cgc gat 432
Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp
130 135 140

gca caa att gtt gac gaa tta acc ggc gag aaa tca gac cgt ttc tta 480
Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu
145 150 155 160

ttc cac tat aac ttc cct ccg tac tct gtc ggt gaa acc ggt cgt atc 528
Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile
165 170 175

ggg tcg ccg aaa cgt cgt gaa atc ggc cac ggt cgt tta gcg aaa cgc 576
Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg
180 185 190

ggg gta tta gcg gta atg ccg act gct gaa gaa ttc ccg tat gta gtg 624
Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val
195 200 205

cgc gta gta tct gaa att acc gaa tca aac ggt tct tct tca atg gct 672
Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala
210 215 220

tcc gta tgc ggc gca tct tta gcg tta atg gac gca ggc gta ccg att 720
Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile
225 230 235 240

aaa gcg gcg gtt gcg ggt atc gca atg ggc tta gtg aaa gaa gaa gaa 768
Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu

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| 245   | 250 | 255 |      |
|---|-----|-----|------|
| aaa ttt gtg gtg ctt tca gac atc tta ggt gac gaa gac cat tta ggc |     |     | 816  |
| Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly |     |     |      |
| 260   | 265 | 270 |      |
| gat atg gac ttc aaa gta gcc ggt acg cgt gaa ggt gta acc gca ctt |     |     | 864  |
| Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu |     |     |      |
| 275   | 280 | 285 |      |
| caa atg gat att aaa atc gaa ggt atc acg cct gaa att atg caa atc |     |     | 912  |
| Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile |     |     |      |
| 290   | 295 | 300 |      |
| gca tta aat caa gcg aaa ggt gcg cgt atg cac atc tta agc gtg atg |     |     | 960  |
| Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met |     |     |      |
| 305   | 310 | 315 | 320  |
| gaa caa gcg att cct gca cct cgt gcc gat att tcc gat ttt gcg cct |     |     | 1008 |
| Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro |     |     |      |
| 325   | 330 | 335 |      |
| cgt att cat acg atg aag atc gat ccg aag aaa atc aaa gac gtg atc |     |     | 1056 |
| Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile |     |     |      |
| 340   | 345 | 350 |      |
| ggt aaa ggc ggt gcg gtt at                                      |     |     | 1076 |
| Gly Lys Gly Gly Ala Val   |     |     |      |
| 355   |     |     |      |

&lt;210&gt; 155

&lt;211&gt; 358

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 155

|   |     |     |    |
|---|-----|-----|----|
| Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp |     |     |    |
| 1   | 5   | 10  | 15 |
| Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu |     |     |    |
| 20  | 25  | 30  |    |
| Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala |     |     |    |
| 35  | 40  | 45  |    |
| Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu |     |     |    |
| 50  | 55  | 60  |    |
| Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile |     |     |    |
| 65  | 70  | 75  | 80 |
| Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu |     |     |    |
| 85  | 90  | 95  |    |
| Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile |     |     |    |
| 100   | 105 | 110 |    |
| Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg |     |     |    |
| 115   | 120 | 125 |    |
| Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp |     |     |    |

| 130                     | 135                     | 140                     |     |
|-------------------------|-------------------------|-------------------------|-----|
| Ala Gln Ile Val Asp     | Glu Leu Thr Gly Glu     | Lys Ser Asp Arg Phe Leu |     |
| 145                     | 150                     | 155                     | 160 |
| Phe His Tyr Asn Phe     | Pro Pro Tyr Ser Val     | Gly Glu Thr Gly Arg Ile |     |
| 165                     | 170                     | 175                     |     |
| Gly Ser Pro Lys Arg Arg | Glu Ile Gly His Gly Arg | Leu Ala Lys Arg         |     |
| 180                     | 185                     | 190                     |     |
| Gly Val Leu Ala Val Met | Pro Thr Ala Glu Glu Phe | Pro Tyr Val Val         |     |
| 195                     | 200                     | 205                     |     |
| Arg Val Val Ser Glu Ile | Thr Glu Ser Asn Gly     | Ser Ser Ser Met Ala     |     |
| 210                     | 215                     | 220                     |     |
| Ser Val Cys Gly Ala Ser | Leu Ala Leu Met Asp     | Ala Gly Val Pro Ile     |     |
| 225                     | 230                     | 235                     | 240 |
| Lys Ala Ala Val Ala Gly | Ile Ala Met Gly Leu     | Val Lys Glu Glu Glu     |     |
| 245                     | 250                     | 255                     |     |
| Lys Phe Val Val Leu Ser | Asp Ile Leu Gly Asp     | Glu Asp His Leu Gly     |     |
| 260                     | 265                     | 270                     |     |
| Asp Met Asp Phe Lys Val | Ala Gly Thr Arg Glu     | Gly Val Thr Ala Leu     |     |
| 275                     | 280                     | 285                     |     |
| Gln Met Asp Ile Lys Ile | Glu Gly Ile Thr Pro     | Glu Ile Met Gln Ile     |     |
| 290                     | 295                     | 300                     |     |
| Ala Leu Asn Gln Ala Lys | Gly Ala Arg Met His     | Ile Leu Ser Val Met     |     |
| 305                     | 310                     | 315                     | 320 |
| Glu Gln Ala Ile Pro Ala | Pro Arg Ala Asp Ile     | Ser Asp Phe Ala Pro     |     |
| 325                     | 330                     | 335                     |     |
| Arg Ile His Thr Met Lys | Ile Asp Pro Lys Lys     | Ile Lys Asp Val Ile     |     |
| 340                     | 345                     | 350                     |     |
| Gly Lys Gly Gly Ala Val |                         |                         |     |
| 355                     |                         |                         |     |

&lt;210&gt; 156

&lt;211&gt; 1055

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; potD

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1053)

&lt;400&gt; 156

|   |    |
|---|----|
| atg aaa aaa tta gcg ggt tta ttt gca gca ggt tta gcg aca gtt gca | 48 |
| Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala |    |
| 1 5 10 15   |    |

|   |    |
|---|----|
| tta aca gcg tgt aat gaa gaa aag cca aaa gcg gct gaa gca gcg gct | 96 |
|---|----|

|   |     |
|---|-----|
| Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala |     |
| 20 25 30  |     |
| caa ccg gca gca gcg gga aca gtt cac ctt tat act tgg act gaa tat | 144 |
| Gln Pro Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr     |     |
| 35 40 45  |     |
| gtg cct gaa ggc ttg tta gat gaa ttt aca aag caa acc ggt atc aaa | 192 |
| Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys |     |
| 50 55 60  |     |
| gta gag gtt tca agc ctt gaa tct aac gaa acc atg tat gcg aaa tta | 240 |
| Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu |     |
| 65 70 75 80   |     |
| aaa tta caa ggt aaa gac ggc ggt tac gat gtt atc gca cct tct aac | 288 |
| Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn |     |
| 85 90 95  |     |
| tac ttc gtt tca aaa atg gcg aaa gaa ggt atg tta gcg gaa tta gat | 336 |
| Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp |     |
| 100 105 110   |     |
| cac gca aaa ctt cct gta atc aaa gag tta aac caa gat tgg tta aac | 384 |
| His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn |     |
| 115 120 125   |     |
| aaa cct tat gac caa ggt aac aaa tac tct tta ccg caa tta tta ggt | 432 |
| Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly |     |
| 130 135 140   |     |
| gca ccg ggt atc gca ttt aac tca aat gac tat aag ggc gat gcg ttc | 480 |
| Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe |     |
| 145 150 155 160   |     |
| act tct tgg ggt gat tta tgg aaa cct gag ttt gcg aat aaa gta caa | 528 |
| Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln |     |
| 165 170 175   |     |
| tta tta gat gac gca cgt gaa gta ttt aac att gcg tta tta aaa tta | 576 |
| Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu |     |
| 180 185 190   |     |
| ggt aaa aac cct aat aca acc aat ccg gaa gag att aaa gcg gct tac | 624 |
| Gly Lys Asn Pro Asn Thr Thr Asn Pro Glu Glu Ile Lys Ala Ala Tyr |     |
| 195 200 205   |     |
| gaa gag tta aga aaa tta cgt cca aac gta ctt tct ttc act tca gac | 672 |
| Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp |     |
| 210 215 220   |     |
| aac cca gcg aac tca ttt atc gca ggt gaa gta tct gta ggt caa tta | 720 |
| Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu |     |
| 225 230 235 240   |     |
| tgg aac ggt tct gta cgt att gcg aaa aaa gaa caa gcg ccg gta aac | 768 |
| Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn |     |
| 245 250 255   |     |
| atg gtg ttc cca aaa gaa ggt cct gta ctt tgg gtt gat acg tta gcc | 816 |
| Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala |     |

| 260   | 265 | 270 |      |
|---|-----|-----|------|
| att ccg gcg aat gcg aaa aac aaa gaa aat gcg cat aag tta atc aac |     |     | 864  |
| Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn |     |     |      |
| 275   | 280 | 285 |      |
| tac tta tta agc gca ccg gtt gcg gaa aaa tta acg tta gaa atc ggt |     |     | 912  |
| Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly |     |     |      |
| 290   | 295 | 300 |      |
| tat ccg act tca aac gta gaa gcg tta aaa aca tta cca aaa gag att |     |     | 960  |
| Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile |     |     |      |
| 305   | 310 | 315 | 320  |
| acc gaa gat ccg gca atc tat ccg aca gct gat gtg tta aaa gcg gca |     |     | 1008 |
| Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala |     |     |      |
| 325   | 330 | 335 |      |
| caa tgg caa gac gat gta ggt aat gca atc gaa ctt tac gaa aaa ta  |     |     | 1055 |
| Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys     |     |     |      |
| 340   | 345 | 350 |      |

&lt;210&gt; 157

&lt;211&gt; 351

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 157

|   |
|---|
| Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala |
| 1 5 10 15   |

|   |
|---|
| Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala |
| 20 25 30  |

|   |
|---|
| Gln Pro Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr |
| 35 40 45  |

|   |
|---|
| Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys |
| 50 55 60  |

|   |
|---|
| Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu |
| 65 70 75 80   |

|   |
|---|
| Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn |
| 85 90 95  |

|   |
|---|
| Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp |
| 100 105 110   |

|   |
|---|
| His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn |
| 115 120 125   |

|   |
|---|
| Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly |
| 130 135 140   |

|   |
|---|
| Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe |
| 145 150 155 160   |

|   |
|---|
| Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln |
| 165 170 175   |

|   |
|---|
| Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu |
|---|

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Gly | Lys | Asn | Pro | Asn | Thr | Thr | Asn | Pro | Glu | Glu | Ile | Lys | Ala | Ala | Tyr |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Glu | Glu | Leu | Arg | Lys | Leu | Arg | Pro | Asn | Val | Leu | Ser | Phe | Thr | Ser | Asp |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Asn | Pro | Ala | Asn | Ser | Phe | Ile | Ala | Gly | Glu | Val | Ser | Val | Gly | Gln | Leu |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Trp | Asn | Gly | Ser | Val | Arg | Ile | Ala | Lys | Lys | Glu | Gln | Ala | Pro | Val | Asn |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Met | Val | Phe | Pro | Lys | Glu | Gly | Pro | Val | Leu | Trp | Val | Asp | Thr | Leu | Ala |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Ile | Pro | Ala | Asn | Ala | Lys | Asn | Lys | Glu | Asn | Ala | His | Lys | Leu | Ile | Asn |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Tyr | Leu | Leu | Ser | Ala | Pro | Val | Ala | Glu | Lys | Leu | Thr | Leu | Glu | Ile | Gly |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Tyr | Pro | Thr | Ser | Asn | Val | Glu | Ala | Leu | Lys | Thr | Leu | Pro | Lys | Glu | Ile |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     | 320 |     |  |
| Thr | Glu | Asp | Pro | Ala | Ile | Tyr | Pro | Thr | Ala | Asp | Val | Leu | Lys | Ala | Ala |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Gln | Trp | Gln | Asp | Asp | Val | Gly | Asn | Ala | Ile | Glu | Leu | Tyr | Glu | Lys |     |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |

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<210> 158
<211> 525
<212> DNA
<213> Actinobacillus pleuropneumoniae
```

```
<220>
<223> rpmF

<220>
<221> CDS
<222> (1) .. (522)
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|       |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> | 158 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| atg   | caa | aag | gta | aaa | cta | ccc | ctc | acc | att | gac | cca | tat | aaa | gac | gct | 48  |  |
| Met   | Gln | Lys | Val | Lys | Leu | Pro | Leu | Thr | Ile | Asp | Pro | Tyr | Lys | Asp | Ala |     |  |
| 1     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |  |
|       |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| cag   | cgt | cga | atg | gat | tac | gaa | ggc | tac | atc | tca | cgt | agt | ctg | ctt | aat | 96  |  |
| Gln   | Arg | Arg | Met | Asp | Tyr | Glu | Gly | Tyr | Ile | Ser | Arg | Ser | Leu | Leu | Asn |     |  |
|       |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |  |
|       |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| cgt   | ttg | ggg | gaa | tct | gtg | agc | aat | gtg | cta | agc | gat | gca | caa | gtt | act | 144 |  |
| Arg   | Leu | Gly | Glu | Ser | Val | Ser | Asn | Val | Leu | Ser | Asp | Ala | Gln | Val | Thr |     |  |
|       |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |  |
|       |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| ctc   | tcg | tta | tat | atc | gat | ccg | caa | cgc | tta | acc | gtt | att | aaa | ggg | acg | 192 |  |
| Leu   | Ser | Leu | Tyr | Ile | Asp | Pro | Gln | Arg | Leu | Thr | Val | Ile | Lys | Gly | Thr |     |  |
|       | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |  |
|       |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| gcg   | aca | gtg | gaa | gtg | gaa | ttc | gat | tgc | caa | cga | tgc | ggg | aac | ccg | ttt | 240 |  |

Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe  
65 70 75 80

aca caa acg ctt gac tgt tct ttt tgt ttc agt ccg gtg tcc aat atg 288  
Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met  
85 90 95

gat cag gcg gac aat ttg ccc gaa att tat gaa cca atc gaa gta aac 336  
Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn  
100 105 110

gag ttc ggt gaa gta aat tta cta gat atg atc gaa gat gga ttt atc 384  
Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile  
115 120 125

atc gaa ttg cct cta gtc ccg atg cat agt gaa gaa cac tgt gaa gtg 432  
Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val  
130 135 140

tcc gtg agt gaa cag gtg ttt ggc gaa ttg cct gaa gaa ttg gcg aaa 480  
Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys  
145 150 155 160

aaa cct aac ccg ttc gct gta tta gct aat tta aag aaa aac tag 525  
Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn  
165 170

&lt;210&gt; 159

&lt;211&gt; 174

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 159

Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala  
1 5 10 15

Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn  
20 25 30

Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr  
35 40 45

Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr  
50 55 60

Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe  
65 70 75 80

Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met  
85 90 95

Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn  
100 105 110

Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile  
115 120 125

Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val  
130 135 140

Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys  
145 150 155 160

Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn  
 165 170

<210> 160  
 <211> 1302  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> tig

<220>  
 <221> CDS  
 <222> (1)..(1299)

<400> 160  
 atg tca att tct att gaa act tta gaa ggc tta caa cgc cgc gta act 48  
 Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr  
 1 5 10 15  
 att acc gta gct gct gat aaa atc gaa gcg gct tac aaa gag caa tta 96  
 Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu  
 20 25 30  
 aaa ggc tat gcg aaa aac gct cgt gta gac ggt ttc cgt aaa ggt aaa 144  
 Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys  
 35 40 45  
 gta ccg cac gca att atc gaa caa cgt ttc ggt tta gcg gct cgc caa 192  
 Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln  
 50 55 60  
 gac gta tta tcc gat gaa atg caa cgt gcg ttc ttt gat gcg gta atc 240  
 Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile  
 65 70 75 80  
 gct gag aaa att aac ctt gcc ggt cgt cct acc ttc aca ccg aac aac 288  
 Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn  
 85 90 95  
 tac caa ccg agt caa gaa ttc agc ttc act gca act ttt gaa gta ttc 336  
 Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe  
 100 105 110  
 ccg gaa gtt gaa tta aaa ggc tta gaa aat atc gaa gtt gaa aaa ccg 384  
 Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro  
 115 120 125  
 gtt gta gaa atc aca gaa gct gat tta gac aaa atg atc gat gtg tta 432  
 Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu  
 130 135 140  
 cgt aaa caa caa gcg act tgg gct gaa tct caa gca gcg gca caa gcg 480  
 Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala  
 145 150 155 160  
 gaa gac cgt gtt gta atc gac ttc gta ggt tct gta gac ggt gaa gag 528  
 Glu Asp Arg Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu  
 165 170 175  
 ttt gaa ggc ggt aaa gcg aca gac ttc act tta gca atg ggt caa agt 576  
 Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser

| 180   |      |  |  |  | 185 |  |  |  |  | 190 |  |  |  |  |  |
|---|------|--|--|--|-----|--|--|--|--|-----|--|--|--|--|--|
| cgt atg atc cct ggt ttt gaa gaa ggt atc gtt ggt cac aaa gcc ggc | 624  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 195   | 200  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| gaa caa ttc gat atc gat gtt act ttc cct gaa gaa tac cac gct gaa | 672  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 210   | 215  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| aac tta aaa ggt aaa gcg gcg aaa ttc gca att aca ctt aag aaa gta | 720  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 225   | 230  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| gaa aat atc gta tta cct gaa tta acc gaa gaa ttc gtg aaa aaa ttc | 768  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 245   | 250  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| ggg tca gca aaa act gta gaa gat tta cgt gcg gaa att aag aaa aat | 816  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 260   | 265  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| atg caa cgt gaa ctt aaa aac gca gta acc gca cgc gtt aaa aac caa | 864  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 275   | 280  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| gta atc aac ggt tta atc gca caa aat gaa att gaa gtg ccg gct gca | 912  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 290   | 295  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| gcg gta gcg gaa gaa gtg gac gta tta cgt cgt caa gcg gtt caa cgt | 960  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 305   | 310  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| ttc ggt ggt aaa ccg gaa atg gct gca caa tta ccg gcg gaa tta ttc | 1008 |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 325   | 330  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| gaa gcg gat gca aaa cgt cgt gtt caa gta ggt tta tta ctt tca acc | 1056 |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 340   | 345  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| gta atc ggt act aac gaa tta aaa gtt gat gaa aaa cgt gtt gaa gaa | 1104 |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 355   | 360  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| acg att gca gaa atc gct tca gct tac gaa caa ccg gcg gaa gtt gtt | 1152 |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 370   | 375  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| gct cat tat gcg aaa aac cgt caa tta acc gaa aat atc cgt aac gta | 1200 |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 385   | 390  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| gtg tta gaa gag caa gcg gtt gaa gtt gta ctt gcg aaa gca aaa gta | 1248 |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 405   | 410  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| act gaa aaa gcg act tct ttt gat gaa gta atg gct caa caa gct caa | 1296 |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln |      |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| 420   | 425  |  |  |  |     |  |  |  |  |     |  |  |  |  |  |
| ggc taa   | 1302 |  |  |  |     |  |  |  |  |     |  |  |  |  |  |



Gly

&lt;210&gt; 161

&lt;211&gt; 433

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 161

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Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr
 1           5           10           15

Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
          20           25           30

Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
          35           40           45

Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
          50           55           60

Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
          65           70           75           80

Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn
          85           90           95

Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe
          100          105          110

Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro
          115          120          125

Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu
          130          135          140

Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala
          145          150          155          160

Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu
          165          170          175

Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser
          180          185          190

Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly
          195          200          205

Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu
          210          215          220

Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val
          225          230          235          240

Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe
          245          250          255

Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn
          260          265          270

Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln
          275          280          285

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Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala  
 290 295 300  
 Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg  
 305 310 315 320  
 Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe  
 325 330 335  
 Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr  
 340 345 350  
 Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu  
 355 360 365  
 Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val  
 370 375 380  
 Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val  
 385 390 395 400  
 Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val  
 405 410 415  
 Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln  
 420 425 430

Gly

<210> 162  
 <211> 316  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> tRNA-glu

<400> 162  
 aatattgcgc tcaaatggca aagcggagag catctttaaa tgttggtcccc atcgtctaga 60  
 ggcctaggac atcgcccttt caccggcgta accgggggttc gaatccccgt ggggacgccca 120  
 tttaaagatg acttttggtg tctgaattgt tctttaaaaa attggaaaca agctgaaaac 180  
 tgagagattt tcgaaagaaa gtctgagtag taaaagataa gtaattatct tgaaaatctt 240  
 agctgaacaa aagcagctaa gtgttttagtt gaataaagta tcgcgttgaa tgcgttcaaa 300  
 taaaatttga aaatat 316

<210> 163  
 <211> 85  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> tRNA-leu

<400> 163  
 gctctgggtg tggaattggt agacacgcta tcttgagggg gtagtgtcca taggatgtgc 60

gagttcgagt ctgcccaga gcacc

85

&lt;210&gt; 164

&lt;211&gt; 623

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; yaeE

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (621)

&lt;400&gt; 164

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | caa | gaa | ctc | aca | cct | caa | atg | tgg | ggc | tta | gtc | ggc | act | tca | acg | 48  |
| Met | Gln | Glu | Leu | Thr | Pro | Gln | Met | Trp | Gly | Leu | Val | Gly | Thr | Ser | Thr |     |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     | 15  |     |     |     |     |
| ctt | gaa | acg | ctc | tat | atg | ggc | ttt | gcg | gcg | act | tta | ctt | gct | gtg | gta | 96  |
| Leu | Glu | Thr | Leu | Tyr | Met | Gly | Phe | Ala | Ala | Thr | Leu | Leu | Ala | Val | Val |     |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     | 30  |     |     |     |     |
| gtc | ggt | ttg | ccg | atc | ggt | ttt | ctg | gca | ttt | tta | acc | ggt | aaa | gga | gag | 144 |
| Val | Gly | Leu | Pro | Ile | Gly | Phe | Leu | Ala | Phe | Leu | Thr | Gly | Lys | Gly | Glu |     |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |     |
| att | tta | gag | aat | ccg | cgt | tta | cat | caa | gta | tta | gat | gtg | att | att | aat | 192 |
| Ile | Leu | Glu | Asn | Pro | Arg | Leu | His | Gln | Val | Leu | Asp | Val | Ile | Ile | Asn |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| atc | ggt | cgt | tcc | gta | ccg | ttt | att | att | ttg | tta | gtc | gtg | ttg | tta | cct | 240 |
| Ile | Gly | Arg | Ser | Val | Pro | Phe | Ile | Ile | Leu | Leu | Val | Val | Leu | Leu | Pro |     |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |
| ttt | acg | cgt | tta | ttg | gtc | ggg | aca | acg | ctc | ggt | act | acg | gcg | gcg | att | 288 |
| Phe | Thr | Arg | Leu | Leu | Val | Gly | Thr | Thr | Leu | Gly | Thr | Thr | Ala | Ala | Ile |     |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| gtg | ccg | tta | agc | gtt | tcg | gca | att | ccg | ttt | ttt | gcg | cgt | tta | act | tca | 336 |
| Val | Pro | Leu | Ser | Val | Ser | Ala | Ile | Pro | Phe | Phe | Ala | Arg | Leu | Thr | Ser |     |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| aat | gcg | tta | tta | gaa | atc | cca | gca | ggt | tta | acc | gaa | gcg | gcg | aaa | tcg | 384 |
| Asn | Ala | Leu | Leu | Glu | Ile | Pro | Ala | Gly | Leu | Thr | Glu | Ala | Ala | Lys | Ser |     |
|     | 115 |     |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| atg | ggc | gca | acg | aat | tgg | caa | gtg | gtc | agt | aaa | ttt | tat | tta | ccg | gaa | 432 |
| Met | Gly | Ala | Thr | Asn | Trp | Gln | Val | Val | Ser | Lys | Phe | Tyr | Leu | Pro | Glu |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| tca | ctg | ccg | att | tta | atc | aat | ggt | atc | aca | tta | act | tta | gtc | gct | tta | 480 |
| Ser | Leu | Pro | Ile | Leu | Ile | Asn | Gly | Ile | Thr | Leu | Thr | Leu | Val | Ala | Leu |     |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| atc | ggt | tat | tcg | gca | atg | gcg | ggt | gcg | gtc | ggc | ggc | ggc | ggt | ttg | ggt | 528 |
| Ile | Gly | Tyr | Ser | Ala | Met | Ala | Gly | Ala | Val | Gly | Gly | Gly | Gly | Leu | Gly |     |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| aac | ctt | gcc | atc | agt | tac | ggt | gaa | cac | cga | aat | atg | gtc | tat | gta | aaa | 576 |
| Asn | Leu | Ala | Ile | Ser | Tyr | Gly | Glu | His | Arg | Asn | Met | Val | Tyr | Val | Lys |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |

tgg atc tca aca att att atc gta gcg att gtg atg atc agt caa aa 623  
 Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met Ile Ser Gln  
           195                          200                          205

<210> 165

<211> 207

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 165

Met Gln Glu Leu Thr Pro Gln Met Trp Gly Leu Val Gly Thr Ser Thr  
       1                          5                          10                          15

Leu Glu Thr Leu Tyr Met Gly Phe Ala Ala Thr Leu Leu Ala Val Val  
           20                          25                          30

Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu  
           35                          40                          45

Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn  
       50                          55                          60

Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro  
       65                          70                          75                          80

Phe Thr Arg Leu Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile  
           85                          90                          95

Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala Arg Leu Thr Ser  
           100                          105                          110

Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr Glu Ala Ala Lys Ser  
       115                          120                          125

Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys Phe Tyr Leu Pro Glu  
       130                          135                          140

Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr Leu Val Ala Leu  
       145                          150                          155                          160

Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly Gly Gly Leu Gly  
           165                          170                          175

Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met Val Tyr Val Lys  
           180                          185                          190

Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met Ile Ser Gln  
       195                          200                          205

<210> 166

<211> 866

<212> DNA

<213> Pasteurella (Mannheimia) haemolytica

<220>

<221> CDS

<222> (1)..(864)

<220>

<223> atpG

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<400> 166
atg gca ggt gct aaa gag ata aga acc aaa att gca agt gtt cgt aat 48
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Arg Asn
1 5 10 15

aca caa aaa att acc aaa gcg atg gaa atg gtt gcc gca tca aaa atg 96
Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys Met
20 25 30

cgt aaa acc caa gag cgt atg gcg gct tct cgc cct tat gct gaa agt 144
Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ala Glu Ser
35 40 45

att cgc aag gca att agc cat att gcc aaa ggt aac att gag tat aaa 192
Ile Arg Lys Ala Ile Ser His Ile Ala Lys Gly Asn Ile Glu Tyr Lys
50 55 60

cac cca ttt ttg acc cca cgt ccg gta aaa aaa gtt ggc tat tta gta 240
His Pro Phe Leu Thr Pro Arg Pro Val Lys Lys Val Gly Tyr Leu Val
65 70 75 80

gtt tca acc gat cgc ggt tta tgt ggt ggc tta aat atc aat tta ttt 288
Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe
85 90 95

aaa acc gtt tta cat gaa ttg aaa gaa aaa gat gac caa ggt gtt aag 336
Lys Thr Val Leu His Glu Leu Lys Glu Lys Asp Asp Gln Gly Val Lys
100 105 110

tct cga ctt gct gtg gtg gga aat aaa ggg atc tcc ttt ttt aac cca 384
Ser Arg Leu Ala Val Val Gly Asn Lys Gly Ile Ser Phe Phe Asn Pro
115 120 125

atg ggg cta gag att aaa ggt cat atc aat gga ttg ggt gat aca ccg 432
Met Gly Leu Glu Ile Lys Gly His Ile Asn Gly Leu Gly Asp Thr Pro
130 135 140

gca atg gaa gat tta gtc ggt att gtt aat ggt atg gta aat gcc tac 480
Ala Met Glu Asp Leu Val Gly Ile Val Asn Gly Met Val Asn Ala Tyr
145 150 155 160

cgt gaa ggc gaa att gat gaa gtg tat gtg gta tat aac cgt ttt ata 528
Arg Glu Gly Glu Ile Asp Glu Val Tyr Val Val Tyr Asn Arg Phe Ile
165 170 175

aac acg atg tca caa aaa ccg aca gta caa cag ttg ctt cct ttg cct 576
Asn Thr Met Ser Gln Lys Pro Thr Val Gln Gln Leu Leu Pro Leu Pro
180 185 190

gca ctg gaa aat gac tca tta gag caa act ggt tct tgg gat tat ctc 624
Ala Leu Glu Asn Asp Ser Leu Glu Gln Thr Gly Ser Trp Asp Tyr Leu
195 200 205

tat gaa cca aat cca caa gcg tta tta gac agc tta ctg gtt cgt tat 672
Tyr Glu Pro Asn Pro Gln Ala Leu Leu Asp Ser Leu Leu Val Arg Tyr
210 215 220

tta gaa tct caa gtt tat cag gca gtg gta gat aat ctt gcg tct gaa 720
Leu Glu Ser Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu
225 230 235 240

cag gct gct cga atg gtg gca atg aaa gca gca acc gat aac gca ggt 768
Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly

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                245                250                255
aat ctg att aat gag tta cag tta gtg tat aac aaa gct cgt caa gca 816
Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala
                260                265                270

agt att acg aat gaa tta aat gaa att gtc gcg ggt gcc gca gca att 864
Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile
                275                280                285

ta 866

<210> 167
<211> 288
<212> PRT
<213> Pasteurella (Mannheimia) haemolytica

<400> 167
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Arg Asn
  1          5          10          15

Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys Met
          20          25          30

Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ala Glu Ser
          35          40          45

Ile Arg Lys Ala Ile Ser His Ile Ala Lys Gly Asn Ile Glu Tyr Lys
          50          55          60

His Pro Phe Leu Thr Pro Arg Pro Val Lys Lys Val Gly Tyr Leu Val
          65          70          75          80

Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe
          85          90          95

Lys Thr Val Leu His Glu Leu Lys Glu Lys Asp Asp Gln Gly Val Lys
          100          105          110

Ser Arg Leu Ala Val Val Gly Asn Lys Gly Ile Ser Phe Phe Asn Pro
          115          120          125

Met Gly Leu Glu Ile Lys Gly His Ile Asn Gly Leu Gly Asp Thr Pro
          130          135          140

Ala Met Glu Asp Leu Val Gly Ile Val Asn Gly Met Val Asn Ala Tyr
          145          150          155          160

Arg Glu Gly Glu Ile Asp Glu Val Tyr Val Val Tyr Asn Arg Phe Ile
          165          170          175

Asn Thr Met Ser Gln Lys Pro Thr Val Gln Gln Leu Leu Pro Leu Pro
          180          185          190

Ala Leu Glu Asn Asp Ser Leu Glu Gln Thr Gly Ser Trp Asp Tyr Leu
          195          200          205

Tyr Glu Pro Asn Pro Gln Ala Leu Leu Asp Ser Leu Leu Val Arg Tyr
          210          215          220

Leu Glu Ser Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu
          225          230          235          240

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Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly  
                             245                            250                            255

Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala  
                             260                            265                            270

Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile  
                             275                            280                            285

<210> 168

<211> 1463

<212> DNA

<213> Pasteurella (Mannheimia) haemolytica

<220>

<221> CDS

<222> (1)..(1461)

<220>

<223> guaB

<400> 168

|  |     |
|--|-----|
| atg cta cga att aaa caa gaa gcc ctc act ttt gat gat gtt ctt ctc                                  | 48  |
| Met Leu Arg Ile Lys Gln Glu Ala Leu Thr Phe Asp Asp Val Leu Leu                                  |     |
| 1                            5                            10                            15       |     |
| gtc ccg gca cat tct act gtg ctt cct aat act gct gat ctt tct act                                  | 96  |
| Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr                                  |     |
| 20                            25                            30                                   |     |
| caa tta act aaa acc att cgt tta aac att ccg atg ctt tct gct gca                                  | 144 |
| Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala                                  |     |
| 35                            40                            45                                   |     |
| atg gat acc gtt aca gaa act aag ctt gcg atc tcc ctt gct caa gaa                                  | 192 |
| Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu                                  |     |
| 50                            55                            60                                   |     |
| ggc ggc att ggt ttt atc cat aaa aat atg tcg att gaa cgc cag gca                                  | 240 |
| Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala                                  |     |
| 65                            70                            75                            80     |     |
| gac cgt gtg cgt aaa gtg aaa aaa ttt gaa agt ggt att gtt tct gag                                  | 288 |
| Asp Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Glu                                  |     |
| 85                            90                            95                                   |     |
| cca gtg acg att tct cct gat atg aca tta gcg gaa ttg gct gaa ttg                                  | 336 |
| Pro Val Thr Ile Ser Pro Asp Met Thr Leu Ala Glu Leu Ala Glu Leu                                  |     |
| 100                            105                            110                                |     |
| gtg aaa aag aac ggt ttt gca ggc tat ccg gtg att gat gaa aac caa                                  | 384 |
| Val Lys Lys Asn Gly Phe Ala Gly Tyr Pro Val Ile Asp Glu Asn Gln                                  |     |
| 115                            120                            125                                |     |
| aat tta gtg gga att att acc gga cgt gat acc cga ttt gtc acg gat                                  | 432 |
| Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp                                  |     |
| 130                            135                            140                                |     |
| tta agc aaa aca gtg cgt gaa ttt atg aca cca aaa gac cgt tta gtg                                  | 480 |
| Leu Ser Lys Thr Val Arg Glu Phe Met Thr Pro Lys Asp Arg Leu Val                                  |     |
| 145                            150                            155                            160 |     |

|   |      |
|---|------|
| acg gta aaa gaa aac gca agc cgt gaa gaa att ttc cac tta atg cac | 528  |
| Thr Val Lys Glu Asn Ala Ser Arg Glu Glu Ile Phe His Leu Met His |      |
| 165 170 175   |      |
| gaa cac cga gtg gag aaa gtg ctg gta gtg aat aat gaa ttt cag tta | 576  |
| Glu His Arg Val Glu Lys Val Leu Val Val Asn Asn Glu Phe Gln Leu |      |
| 180 185 190   |      |
| aaa gga atg att acc cta aaa gac tac caa aaa gcg gaa agc aaa ccg | 624  |
| Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ala Glu Ser Lys Pro |      |
| 195 200 205   |      |
| aat gcc tgt aaa gat gag ttt ggg cgt ttg cgt gtg ggg gcg gca gtg | 672  |
| Asn Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val |      |
| 210 215 220   |      |
| gga gcc ggt ccg ggc aat gaa gaa cga att gat gct tta gta aaa gcg | 720  |
| Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala |      |
| 225 230 235 240   |      |
| ggg gtc gat gtg cta tta atc gac tct tcg cac ggg cat tct gaa ggt | 768  |
| Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly |      |
| 245 250 255   |      |
| gta tta caa cgt gtg cgt gaa acc cgt gca aaa tac cct gat tta ccg | 816  |
| Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro |      |
| 260 265 270   |      |
| att gtt gcc ggt aat att gcc act gca gaa gga gcg att gcg tta gct | 864  |
| Ile Val Ala Gly Asn Ile Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala |      |
| 275 280 285   |      |
| gat gca gga gcc agt gct gtg aaa gta gga atc ggc ccg ggt tca att | 912  |
| Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile |      |
| 290 295 300   |      |
| tgt acc acc aga att gta aca ggc gtt ggc gtg cca caa atc acg gca | 960  |
| Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala |      |
| 305 310 315 320   |      |
| atc gca gaa gcg gca gct gcg ctt aaa gaa cga ggc att cct gtg att | 1008 |
| Ile Ala Glu Ala Ala Ala Ala Leu Lys Glu Arg Gly Ile Pro Val Ile |      |
| 325 330 335   |      |
| gct gat ggt gga att cgt tat tca ggc gat att tca aaa gct att gcc | 1056 |
| Ala Asp Gly Gly Ile Arg Tyr Ser Gly Asp Ile Ser Lys Ala Ile Ala |      |
| 340 345 350   |      |
| gcc ggt gca agt tgc gta atg gtc ggt tcg atg ttt gcc ggc aca gaa | 1104 |
| Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu |      |
| 355 360 365   |      |
| gaa gcc ccg ggt gaa att gag ctt tat caa ggc aga gca ttc aaa tcc | 1152 |
| Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser |      |
| 370 375 380   |      |
| tac cgt gga atg gga tca tta ggt gca atg agt aaa ggc tcg tca gat | 1200 |
| Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp |      |
| 385 390 395 400   |      |
| cgc tat ttc caa tct gat aat gcc gcc gac aag ctc gta ccg gaa ggg | 1248 |
| Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly |      |
| 405 410 415   |      |



att gaa ggg cgt atc gct tac aaa ggc tac ttg aaa gaa att atc cac 1296  
 Ile Glu Gly Arg Ile Ala Tyr Lys Gly Tyr Leu Lys Glu Ile Ile His  
                   420                  425                  430  
 caa caa atg ggc ggc tta cgc tcc tgt atg gga tta acc ggc tgt gcc 1344  
 Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala  
                   435                  440                  445  
 act att gaa gaa ctc cgc acc aaa gca gaa ttt gtc cgc att agt ggt 1392  
 Thr Ile Glu Glu Leu Arg Thr Lys Ala Glu Phe Val Arg Ile Ser Gly  
                   450                  455                  460  
 gct ggt att aaa gaa agc cac gtc cac gat gtg aca att acc aaa gaa 1440  
 Ala Gly Ile Lys Glu Ser His Val His Asp Val Thr Ile Thr Lys Glu  
 465                  470                  475                  480  
 gca ccg aac tac cga atg ggt ta 1463  
 Ala Pro Asn Tyr Arg Met Gly  
                   485

&lt;210&gt; 169

&lt;211&gt; 487

&lt;212&gt; PRT

&lt;213&gt; Pasteurella (Mannheimia) haemolytica

&lt;400&gt; 169

Met Leu Arg Ile Lys Gln Glu Ala Leu Thr Phe Asp Asp Val Leu Leu  
   1                  5                  10                  15  
 Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr  
                   20                  25                  30  
 Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala  
                   35                  40                  45  
 Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu  
                   50                  55                  60  
 Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala  
   65                  70                  75                  80  
 Asp Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Glu  
                   85                  90                  95  
 Pro Val Thr Ile Ser Pro Asp Met Thr Leu Ala Glu Leu Ala Glu Leu  
                   100                  105                  110  
 Val Lys Lys Asn Gly Phe Ala Gly Tyr Pro Val Ile Asp Glu Asn Gln  
                   115                  120                  125  
 Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp  
   130                  135                  140  
 Leu Ser Lys Thr Val Arg Glu Phe Met Thr Pro Lys Asp Arg Leu Val  
   145                  150                  155                  160  
 Thr Val Lys Glu Asn Ala Ser Arg Glu Glu Ile Phe His Leu Met His  
                   165                  170                  175  
 Glu His Arg Val Glu Lys Val Leu Val Val Asn Asn Glu Phe Gln Leu  
                   180                  185                  190

Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ala Glu Ser Lys Pro  
 195 200 205  
 Asn Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val  
 210 215 220  
 Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala  
 225 230 235 240  
 Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly  
 245 250 255  
 Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro  
 260 265 270  
 Ile Val Ala Gly Asn Ile Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala  
 275 280 285  
 Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile  
 290 295 300  
 Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala  
 305 310 315 320  
 Ile Ala Glu Ala Ala Ala Leu Lys Glu Arg Gly Ile Pro Val Ile  
 325 330 335  
 Ala Asp Gly Gly Ile Arg Tyr Ser Gly Asp Ile Ser Lys Ala Ile Ala  
 340 345 350  
 Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu  
 355 360 365  
 Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser  
 370 375 380  
 Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp  
 385 390 395 400  
 Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly  
 405 410 415  
 Ile Glu Gly Arg Ile Ala Tyr Lys Gly Tyr Leu Lys Glu Ile Ile His  
 420 425 430  
 Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala  
 435 440 445  
 Thr Ile Glu Glu Leu Arg Thr Lys Ala Glu Phe Val Arg Ile Ser Gly  
 450 455 460  
 Ala Gly Ile Lys Glu Ser His Val His Asp Val Thr Ile Thr Lys Glu  
 465 470 475 480  
 Ala Pro Asn Tyr Arg Met Gly  
 485

&lt;210&gt; 170

&lt;211&gt; 2150

&lt;212&gt; DNA

&lt;213&gt; Pasteurella (Mannheimia) haemolytica

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (2148)

&lt;220&gt;

&lt;223&gt; pnp

&lt;400&gt; 170

|   |     |
|---|-----|
| atg act cca att gta aaa cag ttt aaa tac ggt cag cac acc gtg acc | 48  |
| Met Thr Pro Ile Val Lys Gln Phe Lys Tyr Gly Gln His Thr Val Thr |     |
| 1 5 10 15   |     |
| tta gaa acc ggt gct atc gca cgc caa gca acg gca gca gta atg gca | 96  |
| Leu Glu Thr Gly Ala Ile Ala Arg Gln Ala Thr Ala Ala Val Met Ala |     |
| 20 25 30  |     |
| agt atg gac gac aca acc gta ttt gtt acc gta gta gcg aaa aaa gac | 144 |
| Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys Lys Asp |     |
| 35 40 45  |     |
| gta aaa gaa ggg caa gat ttc ttc cca tta acc gta gat tat caa gag | 192 |
| Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asp Tyr Gln Glu |     |
| 50 55 60  |     |
| cgt act tac gca gcc ggt cgt att ccg ggc ggt ttc ttc aaa cgt gaa | 240 |
| Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys Arg Glu |     |
| 65 70 75 80   |     |
| gga cgt cct agc gaa ggt gaa acc tta atc gct cgc ttg atc gac cgt | 288 |
| Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile Asp Arg |     |
| 85 90 95  |     |
| cct gtg cgt cca ctt ttc cca gaa ggt ttc ttt aac gaa att caa gtg | 336 |
| Pro Val Arg Pro Leu Phe Pro Glu Gly Phe Phe Asn Glu Ile Gln Val |     |
| 100 105 110   |     |
| att gcg acc gta gta tcg gta aac cca caa atc agt cct gat ctg gtt | 384 |
| Ile Ala Thr Val Val Ser Val Asn Pro Gln Ile Ser Pro Asp Leu Val |     |
| 115 120 125   |     |
| gcg atg atc ggt gca tcg gct gcc ctt tca tta tcc ggc gtg ccg ttt | 432 |
| Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val Pro Phe |     |
| 130 135 140   |     |
| aac ggt cca atc ggt gcg gct cgt gtc ggt ttt atc aac gat caa ttc | 480 |
| Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asn Asp Gln Phe |     |
| 145 150 155 160   |     |
| gta tta aac cca acc acc agc gag caa aaa atc agc cgc tta gat tta | 528 |
| Val Leu Asn Pro Thr Thr Ser Glu Gln Lys Ile Ser Arg Leu Asp Leu |     |
| 165 170 175   |     |
| gtg gtt tca ggt aca gac aaa gcc gtg ttg atg gtg gaa tct gaa gcg | 576 |
| Val Val Ser Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser Glu Ala |     |
| 180 185 190   |     |
| gat atc tta acc gaa gag caa atg tta gcg gcg gtg gtg ttc ggc cac | 624 |
| Asp Ile Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe Gly His |     |
| 195 200 205   |     |
| gag caa caa cag gtt gta atc gaa aac atc aaa gaa ttt gtt aaa gaa | 672 |
| Glu Gln Gln Gln Val Val Ile Glu Asn Ile Lys Glu Phe Val Lys Glu |     |
| 210 215 220   |     |

|   |      |
|---|------|
| gcg ggc aaa cca cgt tgg gat tgg gtt gca cca gag cca aat aca gat | 720  |
| Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn Thr Asp |      |
| 225 230 235 240   |      |
| tta atc aac aaa gta aaa gca tta gca gaa aca cgc ctt ggc gat gct | 768  |
| Leu Ile Asn Lys Val Lys Ala Leu Ala Glu Thr Arg Leu Gly Asp Ala |      |
| 245 250 255   |      |
| tat cgt atc gta gaa aaa caa gtt cgt tac gag caa atc gat gcg att | 816  |
| Tyr Arg Ile Val Glu Lys Gln Val Arg Tyr Glu Gln Ile Asp Ala Ile |      |
| 260 265 270   |      |
| aaa gca gag gtg att gca caa ctt acc gca gaa gat gaa act gtt tct | 864  |
| Lys Ala Glu Val Ile Ala Gln Leu Thr Ala Glu Asp Glu Thr Val Ser |      |
| 275 280 285   |      |
| gaa ggg act atc atc gac atc atc acc gca tta gag agc caa atc gtg | 912  |
| Glu Gly Thr Ile Ile Asp Ile Ile Thr Ala Leu Glu Ser Gln Ile Val |      |
| 290 295 300   |      |
| cgt agc cgt att att gca ggc gaa cca cgc att gac ggc cgt acg gtg | 960  |
| Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr Val |      |
| 305 310 315 320   |      |
| gat acc gtg cgt gca ttg gat att tgc acc agt gtg tta cca cgc acc | 1008 |
| Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Ser Val Leu Pro Arg Thr |      |
| 325 330 335   |      |
| cac ggt tct gct ctt ttc acc cgt ggc gaa acc caa gca tta gca gta | 1056 |
| His Gly Ser Ala Leu Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala Val |      |
| 340 345 350   |      |
| gca aca ttg ggc aca gag cgt gat gcc caa atc att gac gaa ttg acc | 1104 |
| Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu Thr |      |
| 355 360 365   |      |
| ggc gaa aaa tct gac cgt ttc tta ttc cac tac aat ttc cct cca tac | 1152 |
| Gly Glu Lys Ser Asp Arg Phe Leu Phe His Tyr Asn Phe Pro Pro Tyr |      |
| 370 375 380   |      |
| tct gtg ggc gaa acc ggt cgt atc ggc tgc cca aaa cgc cgt gaa atc | 1200 |
| Ser Val Gly Glu Thr Gly Arg Ile Gly Ser Pro Lys Arg Arg Glu Ile |      |
| 385 390 395 400   |      |
| ggt cac ggt cgt tta gca aaa cgt ggc gta tta gcc gtg atg cca acc | 1248 |
| Gly His Gly Arg Leu Ala Lys Arg Gly Val Leu Ala Val Met Pro Thr |      |
| 405 410 415   |      |
| gct gaa gag ttc ccg tat gta gtg cgt gtg gtg tct gaa atc act gaa | 1296 |
| Ala Glu Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr Glu |      |
| 420 425 430   |      |
| tct aac ggt tct tct tca atg gca tct gtg tgt ggt gcg tct ctt gcg | 1344 |
| Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu Ala |      |
| 435 440 445   |      |
| ttg atg gac gca ggt gtg cca atc aaa gca gcg gtt gcc ggt atc gca | 1392 |
| Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile Ala |      |
| 450 455 460   |      |
| atg ggg ctc gtg aaa gaa gac gag aaa ttc gtg gta ctt tct gac atc | 1440 |
| Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp Ile |      |
| 465 470 475 480   |      |

tta ggt gat gaa gac cac tta ggc gat atg gac ttt aaa gta gcg gga 1488  
 Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala Gly  
 485 490 495

acc cgt acc ggt gtg act gcg ctg caa atg gac atc aaa atc gaa ggg 1536  
 Thr Arg Thr Gly Val Thr Ala Leu Met Asp Ile Lys Ile Glu Gly  
 500 505 510

atc acc cct gaa att atg cgt att gcc tta aac caa gct aaa ggt gca 1584  
 Ile Thr Pro Glu Ile Met Arg Ile Ala Leu Asn Gln Ala Lys Gly Ala  
 515 520 525

aga atg cac att tta ggt gta atg gaa caa gcc att ccg gca cct cgt 1632  
 Arg Met His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro Arg  
 530 535 540

gca gat att tct gac tat gcc cca cgc att cac aca atg aag atc gat 1680  
 Ala Asp Ile Ser Asp Tyr Ala Pro Arg Ile His Thr Met Lys Ile Asp  
 545 550 555 560

ccg aag aaa atc aaa gat gtg att ggt aaa ggc ggt gca aca att cgt 1728  
 Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile Arg  
 565 570 575

gct tta acc gaa gag acc aat act tct atc gac att gat gat gac ggt 1776  
 Ala Leu Thr Glu Glu Thr Asn Thr Ser Ile Asp Ile Asp Asp Asp Gly  
 580 585 590

acg gtg aaa att gcg gca act gac ggc aat gca gcg aaa gca gta atg 1824  
 Thr Val Lys Ile Ala Ala Thr Asp Gly Asn Ala Ala Lys Ala Val Met  
 595 600 605

gct cgt att gaa gag atc gtt gcc gaa gtg gaa gta aac caa atc tac 1872  
 Ala Arg Ile Glu Glu Ile Val Ala Glu Val Glu Val Asn Gln Ile Tyr  
 610 615 620

aac ggt aaa gta acc cgt gtg gtg gac ttc ggt gca ttc gtt tcc atc 1920  
 Asn Gly Lys Val Thr Arg Val Val Asp Phe Gly Ala Phe Val Ser Ile  
 625 630 635 640

tta ggt ggc aaa gaa ggt tta gtc cac att tca caa atc acc aac gaa 1968  
 Leu Gly Gly Lys Glu Gly Leu Val His Ile Ser Gln Ile Thr Asn Glu  
 645 650 655

cgt gtt gag cgt gta gcg gac tac tta acc gtt ggt caa gaa gta caa 2016  
 Arg Val Glu Arg Val Ala Asp Tyr Leu Thr Val Gly Gln Glu Val Gln  
 660 665 670

gtg aaa gtg gta gaa att gac cgt caa gga cgc att cgt ctg acg atg 2064  
 Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr Met  
 675 680 685

aaa gac atc aat aat acc aac gag gca aat gca gaa gaa act gta gct 2112  
 Lys Asp Ile Asn Asn Thr Asn Glu Ala Asn Ala Glu Glu Thr Val Ala  
 690 695 700

gaa aat gtg gta gaa aca gaa caa gaa aat aat ttc ta 2150  
 Glu Asn Val Val Glu Thr Glu Gln Glu Asn Asn Phe  
 705 710 715

&lt;210&gt; 171

&lt;211&gt; 716

&lt;212&gt; PRT

&lt;213&gt; Pasteurella (Mannheimia) haemolytica

&lt;400&gt; 171

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Met Thr Pro Ile Val Lys Gln Phe Lys Tyr Gly Gln His Thr Val Thr
 1           5           10           15

Leu Glu Thr Gly Ala Ile Ala Arg Gln Ala Thr Ala Ala Val Met Ala
      20           25           30

Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys Lys Asp
      35           40           45

Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asp Tyr Gln Glu
      50           55           60

Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys Arg Glu
      65           70           75           80

Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile Asp Arg
      85           90           95

Pro Val Arg Pro Leu Phe Pro Glu Gly Phe Phe Asn Glu Ile Gln Val
      100          105          110

Ile Ala Thr Val Val Ser Val Asn Pro Gln Ile Ser Pro Asp Leu Val
      115          120          125

Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val Pro Phe
      130          135          140

Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asn Asp Gln Phe
      145          150          155          160

Val Leu Asn Pro Thr Thr Ser Glu Gln Lys Ile Ser Arg Leu Asp Leu
      165          170          175

Val Val Ser Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser Glu Ala
      180          185          190

Asp Ile Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe Gly His
      195          200          205

Glu Gln Gln Gln Val Val Ile Glu Asn Ile Lys Glu Phe Val Lys Glu
      210          215          220

Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn Thr Asp
      225          230          235          240

Leu Ile Asn Lys Val Lys Ala Leu Ala Glu Thr Arg Leu Gly Asp Ala
      245          250          255

Tyr Arg Ile Val Glu Lys Gln Val Arg Tyr Glu Gln Ile Asp Ala Ile
      260          265          270

Lys Ala Glu Val Ile Ala Gln Leu Thr Ala Glu Asp Glu Thr Val Ser
      275          280          285

Glu Gly Thr Ile Ile Asp Ile Ile Thr Ala Leu Glu Ser Gln Ile Val
      290          295          300

Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr Val
      305          310          315          320

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Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Ser Val Leu Pro Arg Thr  
 325 330 335  
 His Gly Ser Ala Leu Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala Val  
 340 345 350  
 Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu Thr  
 355 360 365  
 Gly Glu Lys Ser Asp Arg Phe Leu Phe His Tyr Asn Phe Pro Pro Tyr  
 370 375 380  
 Ser Val Gly Glu Thr Gly Arg Ile Gly Ser Pro Lys Arg Arg Glu Ile  
 385 390 395 400  
 Gly His Gly Arg Leu Ala Lys Arg Gly Val Leu Ala Val Met Pro Thr  
 405 410 415  
 Ala Glu Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr Glu  
 420 425 430  
 Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu Ala  
 435 440 445  
 Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile Ala  
 450 455 460  
 Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp Ile  
 465 470 475 480  
 Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala Gly  
 485 490 495  
 Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu Gly  
 500 505 510  
 Ile Thr Pro Glu Ile Met Arg Ile Ala Leu Asn Gln Ala Lys Gly Ala  
 515 520 525  
 Arg Met His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro Arg  
 530 535 540  
 Ala Asp Ile Ser Asp Tyr Ala Pro Arg Ile His Thr Met Lys Ile Asp  
 545 550 555 560  
 Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile Arg  
 565 570 575  
 Ala Leu Thr Glu Glu Thr Asn Thr Ser Ile Asp Ile Asp Asp Gly  
 580 585 590  
 Thr Val Lys Ile Ala Ala Thr Asp Gly Asn Ala Ala Lys Ala Val Met  
 595 600 605  
 Ala Arg Ile Glu Glu Ile Val Ala Glu Val Glu Val Asn Gln Ile Tyr  
 610 615 620  
 Asn Gly Lys Val Thr Arg Val Val Asp Phe Gly Ala Phe Val Ser Ile  
 625 630 635 640  
 Leu Gly Gly Lys Glu Gly Leu Val His Ile Ser Gln Ile Thr Asn Glu  
 645 650 655

Arg Val Glu Arg Val Ala Asp Tyr Leu Thr Val Gly Gln Glu Val Gln  
660 665 670

Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr Met  
675 680 685

Lys Asp Ile Asn Asn Thr Asn Glu Ala Asn Ala Glu Glu Thr Val Ala  
690 695 700

Glu Asn Val Val Glu Thr Glu Gln Glu Asn Asn Phe  
705 710 715

<210> 172  
<211> 1517  
<212> DNA  
<213> Pasteurella (Mannheimia) haemolytica

<220>  
<221> CDS  
<222> (1)..(1515)

<220>  
<223> purF

<400> 172  
atg tgc ggc att gtc ggt att att ggg aat tcg ccg gtg aat cag gcg 48  
Met Cys Gly Ile Val Gly Ile Ile Gly Asn Ser Pro Val Asn Gln Ala  
1 5 10 15

att tat gat ggt tta aca tta ctt caa cac cga gga caa gat gcc gca 96  
Ile Tyr Asp Gly Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala  
20 25 30

ggt atc gtc acc ata gac gat gaa aat cgt ttc cgc tta cgc aaa gct 144  
Gly Ile Val Thr Ile Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala  
35 40 45

aac ggc tta gtc agc gat gtt ttc cag caa gag cat atg gtg aga tta 192  
Asn Gly Leu Val Ser Asp Val Phe Gln Gln Glu His Met Val Arg Leu  
50 55 60

caa ggc aat gtt gga att ggt cac gtt cgc tac cca aca gca ggt agc 240  
Gln Gly Asn Val Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser  
65 70 75 80

tca agt gtg tct gaa gcc cag cca ttt tat gtc aat tca cct ttc ggt 288  
Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Phe Gly  
85 90 95

att acc tta gtt cac aac ggt aat tta act aat aat gcg gaa ctt aaa 336  
Ile Thr Leu Val His Asn Gly Asn Leu Thr Asn Asn Ala Glu Leu Lys  
100 105 110

gct cgc tta tac aac gaa gcc cgc cgc cat gtg aac act aat tct gat 384  
Ala Arg Leu Tyr Asn Glu Ala Arg Arg His Val Asn Thr Asn Ser Asp  
115 120 125

tct gaa tcc ctt ctt aat att ttt gct tac ttt tta gat ctc tat tcc 432  
Ser Glu Ser Leu Leu Asn Ile Phe Ala Tyr Phe Leu Asp Leu Tyr Ser  
130 135 140

act cag cat tta agc cca gac aat atc ttt gaa acg gtt cgt aaa acc 480



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Thr | Gln | His | Leu | Ser | Pro | Asp | Asn | Ile | Phe | Glu | Thr | Val | Arg | Lys | Thr |      |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |      |  |
| aat | gat | agc | att | cgt | ggg | gct | tat | gct | tgc | att | gcg | atg | att | atc | gga | 528  |  |
| Asn | Asp | Ser | Ile | Arg | Gly | Ala | Tyr | Ala | Cys | Ile | Ala | Met | Ile | Ile | Gly |      |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |      |  |
| cac | ggg | atg | gtt | gct | ttc | cgt | gac | cca | ttc | ggg | att | cgc | ccg | tta | gtg | 576  |  |
| His | Gly | Met | Val | Ala | Phe | Arg | Asp | Pro | Phe | Gly | Ile | Arg | Pro | Leu | Val |      |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |      |  |
| ctg | ggg | aaa | cgt | gaa | atc | gag | ggg | aaa | acc | gaa | tat | atg | ttt | gct | tcg | 624  |  |
| Leu | Gly | Lys | Arg | Glu | Ile | Glu | Gly | Lys | Thr | Glu | Tyr | Met | Phe | Ala | Ser |      |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |      |  |
| gaa | agt | gtg | gct | ctt | gat | gta | gtg | ggg | ttt | gaa | ttt | gtg | cga | gat | gtg | 672  |  |
| Glu | Ser | Val | Ala | Leu | Asp | Val | Val | Gly | Phe | Glu | Phe | Val | Arg | Asp | Val |      |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |      |  |
| ctg | ccg | ggg | gaa | gcg | att | tat | gtt | acc | ttt | gat | ggg | caa | tta | cat | tcg | 720  |  |
| Leu | Pro | Gly | Glu | Ala | Ile | Tyr | Val | Thr | Phe | Asp | Gly | Gln | Leu | His | Ser |      |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |      |  |
| caa | att | tgt | gcc | gat | aat | cca | aaa | ctg | aat | cct | tgt | att | ttt | gaa | tat | 768  |  |
| Gln | Ile | Cys | Ala | Asp | Asn | Pro | Lys | Leu | Asn | Pro | Cys | Ile | Phe | Glu | Tyr |      |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |      |  |
| gtt | tat | ttt | gcc | cgt | cct | gat | tcc | gtc | att | gat | ggc | gtt | tct | gta | tat | 816  |  |
| Val | Tyr | Phe | Ala | Arg | Pro | Asp | Ser | Val | Ile | Asp | Gly | Val | Ser | Val | Tyr |      |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |      |  |
| tct | gca | cga | gtg | cat | atg | ggc | gaa | tta | tta | ggg | gag | aaa | att | aaa | cgt | 864  |  |
| Ser | Ala | Arg | Val | His | Met | Gly | Glu | Leu | Leu | Gly | Glu | Lys | Ile | Lys | Arg |      |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |      |  |
| gaa | tgg | gga | cga | att | atc | gat | gat | att | gat | gtg | gtg | atc | ccg | att | cct | 912  |  |
| Glu | Trp | Gly | Arg | Ile | Ile | Asp | Asp | Ile | Asp | Val | Val | Ile | Pro | Ile | Pro |      |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |      |  |
| gaa | acc | tca | aat | gat | att | gcg | gta | cgt | att | gct | aat | atg | ttg | tat | aaa | 960  |  |
| Glu | Thr | Ser | Asn | Asp | Ile | Ala | Val | Arg | Ile | Ala | Asn | Met | Leu | Tyr | Lys |      |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |      |  |
| ccc | tat | cgt | caa | ggg | ttt | gtt | aaa | aac | cgc | tat | gta | gct | cga | act | ttt | 1008 |  |
| Pro | Tyr | Arg | Gln | Gly | Phe | Val | Lys | Asn | Arg | Tyr | Val | Ala | Arg | Thr | Phe |      |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |      |  |
| att | atg | ccg | ggg | caa | gca | cag | cgt | aaa | agc | tcg | gtt | cgc | cgt | aaa | tta | 1056 |  |
| Ile | Met | Pro | Gly | Gln | Ala | Gln | Arg | Lys | Ser | Ser | Val | Arg | Arg | Lys | Leu |      |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |      |  |
| aat | gcg | att | gcc | tct | gaa | ttt | aaa | ggc | aaa | agc | gtg | tta | ctg | gtt | gat | 1104 |  |
| Asn | Ala | Ile | Ala | Ser | Glu | Phe | Lys | Gly | Lys | Ser | Val | Leu | Leu | Val | Asp |      |  |
|     |     |     | 355 |     |     |     | 360 |     |     |     |     | 365 |     |     |     |      |  |
| gat | tct | att | gta | cga | ggg | aca | acg | tct | gaa | caa | atc | gtg | gaa | atg | gca | 1152 |  |
| Asp | Ser | Ile | Val | Arg | Gly | Thr | Thr | Ser | Glu | Gln | Ile | Val | Glu | Met | Ala |      |  |
|     |     |     | 370 |     |     | 375 |     |     |     |     | 380 |     |     |     |     |      |  |
| cga | gca | gct | ggg | gca | aaa | cgg | gtt | tat | ttt | gcc | tct | gcc | gca | ccg | gaa | 1200 |  |
| Arg | Ala | Ala | Gly | Ala | Lys | Arg | Val | Tyr | Phe | Ala | Ser | Ala | Ala | Pro | Glu |      |  |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |      |  |

att cgc tac ccg aat gtg tat ggc att gat atg ccg act tgt gaa gaa 1248  
 Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Cys Glu Glu  
 405 410 415  
 tta gtg gct tat gat cgc tca gtg gaa gag gtt gca cag atg ata ggg 1296  
 Leu Val Ala Tyr Asp Arg Ser Val Glu Glu Val Ala Gln Met Ile Gly  
 420 425 430  
 gtg gat aaa ttg att ttc caa gac ctt gaa gca ctt tat aag tct att 1344  
 Val Asp Lys Leu Ile Phe Gln Asp Leu Glu Ala Leu Tyr Lys Ser Ile  
 435 440 445  
 caa ctg gaa aat ccg act att cat cgc ttt gat gac tct gta ttt aca 1392  
 Gln Leu Glu Asn Pro Thr Ile His Arg Phe Asp Asp Ser Val Phe Thr  
 450 455 460  
 gga gaa tat att aca ggt gat gta gat aaa tgc tat tta gac agt ata 1440  
 Gly Glu Tyr Ile Thr Gly Asp Val Asp Lys Cys Tyr Leu Asp Ser Ile  
 465 470 475 480  
 gca aga tct cga aac gat aaa gca aaa gca gag gcg gca aaa caa gcc 1488  
 Ala Arg Ser Arg Asn Asp Lys Ala Lys Ala Glu Ala Ala Lys Gln Ala  
 485 490 495  
 acc aat tta gaa att cat aac gaa aga ta 1517  
 Thr Asn Leu Glu Ile His Asn Glu Arg  
 500 505

&lt;210&gt; 173

&lt;211&gt; 505

&lt;212&gt; PRT

&lt;213&gt; Pasteurella (Mannheimia) haemolytica

&lt;400&gt; 173

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 Gly Ile Val Thr Ile Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala  
 35 40 45  
 Asn Gly Leu Val Ser Asp Val Phe Gln Gln Glu His Met Val Arg Leu  
 50 55 60  
 Gln Gly Asn Val Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser  
 65 70 75 80  
 Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Phe Gly  
 85 90 95  
 Ile Thr Leu Val His Asn Gly Asn Leu Thr Asn Asn Ala Glu Leu Lys  
 100 105 110  
 Ala Arg Leu Tyr Asn Glu Ala Arg Arg His Val Asn Thr Asn Ser Asp  
 115 120 125  
 Ser Glu Ser Leu Leu Asn Ile Phe Ala Tyr Phe Leu Asp Leu Tyr Ser  
 130 135 140

Thr Gln His Leu Ser Pro Asp Asn Ile Phe Glu Thr Val Arg Lys Thr  
 145 150 155 160  
 Asn Asp Ser Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly  
 165 170 175  
 His Gly Met Val Ala Phe Arg Asp Pro Phe Gly Ile Arg Pro Leu Val  
 180 185 190  
 Leu Gly Lys Arg Glu Ile Glu Gly Lys Thr Glu Tyr Met Phe Ala Ser  
 195 200 205  
 Glu Ser Val Ala Leu Asp Val Val Gly Phe Glu Phe Val Arg Asp Val  
 210 215 220  
 Leu Pro Gly Glu Ala Ile Tyr Val Thr Phe Asp Gly Gln Leu His Ser  
 225 230 235 240  
 Gln Ile Cys Ala Asp Asn Pro Lys Leu Asn Pro Cys Ile Phe Glu Tyr  
 245 250 255  
 Val Tyr Phe Ala Arg Pro Asp Ser Val Ile Asp Gly Val Ser Val Tyr  
 260 265 270  
 Ser Ala Arg Val His Met Gly Glu Leu Leu Gly Glu Lys Ile Lys Arg  
 275 280 285  
 Glu Trp Gly Arg Ile Ile Asp Asp Ile Asp Val Val Ile Pro Ile Pro  
 290 295 300  
 Glu Thr Ser Asn Asp Ile Ala Val Arg Ile Ala Asn Met Leu Tyr Lys  
 305 310 315 320  
 Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Ala Arg Thr Phe  
 325 330 335  
 Ile Met Pro Gly Gln Ala Gln Arg Lys Ser Ser Val Arg Arg Lys Leu  
 340 345 350  
 Asn Ala Ile Ala Ser Glu Phe Lys Gly Lys Ser Val Leu Leu Val Asp  
 355 360 365  
 Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala  
 370 375 380  
 Arg Ala Ala Gly Ala Lys Arg Val Tyr Phe Ala Ser Ala Ala Pro Glu  
 385 390 395 400  
 Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Cys Glu Glu  
 405 410 415  
 Leu Val Ala Tyr Asp Arg Ser Val Glu Glu Val Ala Gln Met Ile Gly  
 420 425 430  
 Val Asp Lys Leu Ile Phe Gln Asp Leu Glu Ala Leu Tyr Lys Ser Ile  
 435 440 445  
 Gln Leu Glu Asn Pro Thr Ile His Arg Phe Asp Asp Ser Val Phe Thr  
 450 455 460  
 Gly Glu Tyr Ile Thr Gly Asp Val Asp Lys Cys Tyr Leu Asp Ser Ile  
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Ala Arg Ser Arg Asn Asp Lys Ala Lys Ala Glu Ala Ala Lys Gln Ala  
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Thr Asn Leu Glu Ile His Asn Glu Arg  
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<211> 386

<212> DNA

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<400> 174

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gtg caa gca gtt gat tta ggc aat atg gtt tta act tct ggg caa att 96  
 Val Gln Ala Val Asp Leu Gly Asn Met Val Leu Thr Ser Gly Gln Ile  
 20 25 30

ccc gtg aat cct gaa acc ggc gaa atc ccg agt gat att gtg caa caa 144  
 Pro Val Asn Pro Glu Thr Gly Glu Ile Pro Ser Asp Ile Val Gln Gln  
 35 40 45

acc cgc caa tct ctg aac aac gtg aaa gcc att atc gaa caa gcc ggc 192  
 Thr Arg Gln Ser Leu Asn Asn Val Lys Ala Ile Ile Glu Gln Ala Gly  
 50 55 60

tta acc gtt gcc gat att gta aag acc acc gta ttt gtc aaa gat ctt 240  
 Leu Thr Val Ala Asp Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu  
 65 70 75 80

aac gac ttc gca aag gta aat gcg gaa tac caa gcc ttc ttc caa gaa 288  
 Asn Asp Phe Ala Lys Val Asn Ala Glu Tyr Gln Ala Phe Phe Gln Glu  
 85 90 95

aac gaa cac cct aat ttt ccg gct cgt tct tgc gta gaa gtg gct cgt 336  
 Asn Glu His Pro Asn Phe Pro Ala Arg Ser Cys Val Glu Val Ala Arg  
 100 105 110

tta cca aaa gat gtt ggc att gag atc gaa gcg att gca gta cgc cga 384  
 Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala Val Arg Arg  
 115 120 125

ta 386

<210> 175

<211> 128

<212> PRT

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<400> 175

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 1 5 10 15

Val Gln Ala Val Asp Leu Gly Asn Met Val Leu Thr Ser Gly Gln Ile  
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Pro Val Asn Pro Glu Thr Gly Glu Ile Pro Ser Asp Ile Val Gln Gln  
                   35                  40                  45

Thr Arg Gln Ser Leu Asn Asn Val Lys Ala Ile Ile Glu Gln Ala Gly  
           50                  55                  60

Leu Thr Val Ala Asp Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu  
       65                  70                  75                  80

Asn Asp Phe Ala Lys Val Asn Ala Glu Tyr Gln Ala Phe Phe Gln Glu  
                   85                  90                  95

Asn Glu His Pro Asn Phe Pro Ala Arg Ser Cys Val Glu Val Ala Arg  
                   100                  105                  110

Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala Val Arg Arg  
           115                  120                  125

&lt;210&gt; 176

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt;

&lt;222&gt;

&lt;223&gt; Description of Artificial Sequence: PRIMER

&lt;400&gt; 176

atggcnggng cnaargarat

20

&lt;210&gt; 177

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt;

&lt;222&gt;

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&lt;222&gt; 3

&lt;223&gt; n = A or T or G or C

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 12

&lt;223&gt; n = A or T or G or C

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 15

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&lt;400&gt; 177

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&lt;210&gt; 178

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 ggctcagaaa caataccact ttca 24

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gcaccaaagc agaatttgtc c 21

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accatcataa atcgctgat tc 22

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<220>  
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ctgaacaacg tgaaagccat 20

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International Bureau



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26 September 2002 (26.09.2002)

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Published:

— with international search report

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(54) Title: ANTI-BACTERIAL VACCINE COMPOSITIONS

(57) Abstract: Gram negative bacterial virulence genes are identified, thereby allowing the identification of anti-bacterial agents that target these virulence genes and their products, and the provision of gram negative bacterial mutants useful in vaccines.

WO 02/075507 A3



## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 02/01971

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N1/20 A61K39/102 A61K35/74 C12N15/31 C12N15/63  
 C07K14/285 C07K16/12 C12Q1/18 G01N33/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N A61K C07K C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EMBL, EPO-Internal, WPI Data, BIOSIS, MEDLINE

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category ° | Citation of document, with indication, where appropriate, of the relevant passages  | Relevant to claim No. |
|------------|---|-----------------------|
| X          | DATABASE EMBL [Online]<br>10 February 2001 (2001-02-10)<br>MAY B.J. ET AL.: "Pasteurella multocida<br>PM70 section 152 of 204 of the complete<br>genome"<br>Database accession no. AE006064<br>XP002224305<br>nucleotides 3352-4146 | 1-41                  |
| X          | & DATABASE EMBL [Online]<br>Entry AE006064,<br>10 February 2001 (2001-02-10)<br>MAY B.J. ET AL.: "Pasteurella multocida<br>PM70 section 31 of 204 of the complete<br>genome"  | 5-23, 25,<br>28       |
| A          | the whole document<br>& BARBARA J. MAY ET AL.: "Complete<br>genomic sequence of Pasteurella multocida,<br>Pm70"<br>PROCEEDINGS OF THE NATIONAL ACADEMY OF<br>-/--   | 1-41                  |

☒ Further documents are listed in the continuation of box C.☐ Patent family members are listed in annex.

## ° Special categories of cited documents :

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"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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Date of the actual completion of the international search

12 May 2003

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Authorized officer

Montero Lopez, B

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 02/01971

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category ° | Citation of document, with indication, where appropriate, of the relevant passages   | Relevant to claim No.  |
|------------|--|------------------------|
| X          | <p>SCIENCES OF USA,<br/>vol. 98, no. 6,<br/>13 March 2001 (2001-03-13), pages<br/>3460-3465, XP002202785<br/>WASHINGTON US<br/>page 3463, right-hand column, paragraph 2<br/>-page 3464, left-hand column, paragraph 1<br/>---</p> <p>COONEY ET AL: "Three contiguous<br/>lipoprotein genes in Pasteurella<br/>haemolytica A1 which are homologous to a<br/>lipoprotein gene in Haemophilus influenza<br/>Type b"<br/>INFECTION AND IMMUNITY, AMERICAN SOCIETY<br/>OF MICROBIOLOGY, WASHINGTON, DC, US,<br/>vol. 61, no. 11, November 1993 (1993-11),<br/>pages 4682-4688, XP002148894<br/>ISSN: 0019-9567<br/>abstract<br/>page 4683, left-hand column, last<br/>paragraph -page 4685, left-hand column,<br/>paragraph 1; figures 3,4<br/>page 4686, right-hand column, paragraph 2<br/>---</p> | <p>5-23,25,<br/>28</p> |
| A          | <p>---<br/>TROY E. FULLER ET AL.: "Identification of<br/>Pasteurella multocida virulence genes in a<br/>septicemic mouse model using<br/>signature-tagged mutagenesis"<br/>MICROBIAL PATHOGENESIS,<br/>vol. 29, 2000, pages 25-38, XP002224304<br/>the whole document<br/>-----</p>  | <p>1-41</p>            |

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US 02/01971

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:  
1-41 partially
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-41 partially

Gram-negative bacteria comprising a mutation in a gene of sequence SEQ ID NO:1 resulting in decreased activity of the gene product; immunogenic composition comprising the bacteria; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:1, vector and host cell comprising the same and use thereof to produce a polypeptide; encoded polypeptide of sequence SEQ ID NO:2; antibody against it; use of the polypeptide of sequence SEQ ID NO:2 for identifying antibacterial agents.

2. Claims: 1-41 partially

Idem as subject 1 for, respectively sequences SEQ ID NO:3 and 4; 7 and 8; 9 and 10; 21 and 22; 25 and 26.

3. Claims: 1-4, 21-23, 27, 28 partially

Gram-negative bacteria comprising a mutation in a gene of sequence SEQ ID NO:27 resulting in decreased activity of the gene product; immunogenic composition comprising the bacteria; nucleotide sequence comprising SEQ ID NO:27.

4. Claims: 1-41 partially

Idem as subject 1 for, respectively, sequences SEQ ID NOs:29 and 30; 39 and 40; 41 and 42; 51 and 52; 53 and 54; 55 and 56.

5. Claims: 1-28 partially

Gram-negative bacteria comprising a mutation in a gene of sequence SEQ ID NO:57 resulting in decreased activity of the gene product; immunogenic composition comprising the bacteria; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:57.

6. Claims: 1-41 partially

Idem as subject 1 for, respectively sequences SEQ ID NOs:58 and 59; 60 and 61; 68 and 69; 72 and 73; 74 and 75; 76 and 77; 78 and 79; 80 and 81; 82 and 83; 84 and 85; 104 and 105; 108 and 109; 112 and 113; 116 and 117; 118 and 119; 120 and 121; 122 and 123; 124 and 125; 126 and 127; 128 and 129; 130 and 131

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

## 7. Claims: 5-26, 29-41 partially

Attenuated Pasteurellaceae bacteria comprising a mutation in a gene of sequence SEQ ID NO:11; immunogenic composition containing it; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:11, vector and host cell comprising the same and use thereof to produce a polypeptide; encoded polypeptide of sequence SEQ ID NO:12; antibody against it; use of the polypeptide of sequence SEQ ID NO:12 for identifying antibacterial agents.

## 8. Claims: 5-26, 28-41 partially

Idem as subject 36 for, respectively, sequences SEQ ID NOs:13 and 14; 15 and 16; 17 and 18; 19 and 20; 23 and 24; 31 and 32; 33 and 34; 35 and 36; 37 and 38; 70 and 71; 100 and 101; 102 and 103; 106 and 107; 110 and 111; 114 and 115; 132 and 133; 134 and 135; 136 and 137; 138 and 139; 140 and 141; 142 and 143; 144 and 145; 146 and 147; 148 and 149; 150 and 151; 152 and 153; 154 and 155; 156 and 157; 158 and 159; 160 and 161

## 9. Claims: 5-26 partially

Attenuated Pasteurellaceae bacteria comprising a mutation in, respectively a gene of sequence SEQ ID NO:162 and 163; immunogenic composition containing it; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:162 or 163.

## 10. Claims: 5-26, 28-41 partially

Idem as subject 36 for, respectively, sequences SEQ ID NOs:164 and 165; 166 and 167; 168 and 169; 170 and 171; 172 and 173; 174 and 175



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(54) Title: ANTI-BACTERIAL VACCINE COMPOSITIONS

(57) Abstract: Gram negative bacterial virulence genes are identified, thereby allowing the identification of anti-bacterial agents that target these virulence genes and their products, and the provision of gram negative bacterial mutants useful in vaccines.

WO 02/075507 A3



**AMENDED CLAIMS**

[received by the International Bureau on 11 July 2003 (11.07.03)  
original claims 1 to 41 have been amended by claims 1 to 29]

**WHAT IS CLAIMED IS:**

1. An attenuated *Mannheimia* bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOS: 166, 168, 170, 172 and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.
2. The *Mannheimia* bacteria of claim 1 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
3. The *Mannheimia* bacteria of claim 1 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.
4. The *Mannheimia* bacteria of claim 1 wherein said mutation results in deletion of all or part of said gene.
5. The *Mannheimia* bacteria of claim 1 wherein the *Mannheimia* bacteria is *Mannheimia haemolytica*.
6. The *Mannheimia* bacteria of claim 5 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
7. The *Mannheimia* bacteria of claim 5 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.
8. The *Mannheimia* bacteria of claim 5 wherein said mutation results in deletion of all or part of said gene.
9. An immunogenic composition comprising the bacteria according to any one of claims 1 through 8.

10. A vaccine composition comprising the immunogenic composition according to claim 9 and a pharmaceutically acceptable carrier.

5 11. The vaccine composition according to claim 10 further comprising an adjuvant.

12. A method for producing a gram-negative bacteria mutant comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOS: 166, 168, 170, 172, and 174 or a species homolog  
10 thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

13. A method for producing an attenuated *Mannheimia* bacteria comprising the step of introducing a mutation in a gene represented by a nucleotide  
15 sequence set forth in any one of SEQ ID NOS: 166, 168, 170, 172, and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

14. A purified and isolated *Mannheimia* polynucleotide comprising a  
20 nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOS: 166, 168, 170, 172 and 174.

15. A purified and isolated *Mannheimia* polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NO: 166.  
25

16. A purified and isolated polynucleotide encoding a *Mannheimia* virulence gene product, or species homolog thereof, selected from the group consisting of:

a) the polynucleotide according to claim 14;

b) polynucleotides encoding a polypeptide encoded by the polynucleotide of (a); and

c) polynucleotides that hybridize to the complement of the polynucleotides of (a) or (b) under moderate stringency conditions.

5

17. A purified and isolated *Mannheimia* polynucleotide encoding a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOS: 167, 169, 171, 173, and 175.

10

18. The polynucleotide of claim 17 which is a DNA.

19. A vector comprising the DNA of claim 18.

20. The vector of claim 19 that is an expression vector, wherein the DNA  
15 is operatively linked to an expression control DNA sequence.

21. A host cell stably transformed or transfected with the DNA of claim 18 in a manner allowing the expression of the encoded polypeptide in said host cell.

20

22. A method for producing a recombinant polypeptide comprising culturing the host cell of claim 21 in a nutrient medium and isolating the encoded polypeptide from said host cell or said nutrient medium.

23. A purified polypeptide produced by the method of claim 22.

25

24. A purified polypeptide comprising a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOS: 167, 169, 171, 173, and 175.

25. An antibody that is specifically reactive with the polypeptide of claim  
24.

5

26. The antibody of claim 25 that is a monoclonal antibody.

27. A method of using the monoclonal antibody of claim 26 for identifying  
a bacteria of claims 1 or 5, comprising the steps of contacting an extract of bacteria  
with said monoclonal antibody and detecting the absence of binding of said  
monoclonal antibody.

10

28. A method of identifying an anti-bacterial agent comprising the steps of  
assaying potential agents for the ability to interfere with expression or activity of gene  
products represented by the amino acid sequences set forth in any one of SEQ ID  
NOS: 167, 169, 171, 173, and 175 and identifying an agent that interferes with  
15 expression or activity of said gene products.

29. A method of identifying an anti-bacterial agent comprising the steps  
of:

- 20 a) measuring expression or activity of a gene product as set out in  
any one of SEQ ID NOS: 167, 169, 171, 173, and 175;  
b) contacting the gene product in (a) with a test compound;  
c) measuring expression or activity of the gene product in the  
presence of the test compound; and  
d) identifying the test compound as an antibacterial agent when  
25 expression or activity of the gene product is decreased in the presence of the test  
compound as compared to expression or activity in the absence of the test compound.